

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-43821

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1122 CAGTTCACCTTCACCTCC 1140
||| ||||| ||||| |||||
Db 2 CAGGACCACCTTCACCTTC 20

RESULT 704

US-10-266-090-47293
; Sequence 47293, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/336,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47293
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-47293

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1137 CTCGAGCTCCACTATACC 1155
||| ||||| ||||| |||||
Db 2 CTCGACCACCACTTAACC 20

RESULT 705

US-10-289-762-2388
; Sequence 2388, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2388
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2388

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 963 CCAACGGTGAAGTCCAAG 981

||| ||||| ||||| |||||
Db 1 CGAACGGTAGAAATCCAAG 19

RESULT 706

US-10-289-762-4651
; Sequence 4651, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4651

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 758 GCCATGCGAGTTTCTTCT 776
||| ||||| ||||| |||||
Db 2 GCCATGCGAGTTTCTTCT 20

RESULT 707

US-10-289-762-5845/c
; Sequence 5845, Application US/10289762
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5845
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5845

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 816 AAGCCTGGAGTGCACGAAG 834
||| ||||| ||||| |||||
Db 20 AAGCAGGAGTGCACGCAG 2

RESULT 708

US-10-289-845-14/c
; Sequence 14, Application US/10289845
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Wagner, Susanne
; APPLICANT: Parodi, Luis
; TITLE OF INVENTION: Single Nucleotide Polymorphisms in GH-1
; FILE REFERENCE: 00791.US1
; CURRENT APPLICATION NUMBER: US/10/289,845
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20

; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-289-845-14

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1011 ACTGAAAGAGGGGAG 1029
| | | | | | | | | | | | | | | | | | | | | |
Db 19 ATCTGAAAGAGGAGGAG 1

RESULT 709

US-10-293-338-5780/c
; Sequence 5780, Application US/10293338

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics LTD

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND

; FILE REFERENCE: 45282

; CURRENT APPLICATION NUMBER: US/10/293,338

; CURRENT FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 8785

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5780

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-293-338-5780

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1247 CCGACCCCATCCCAACCC 1265
| | | | | | | | | | | | | | | | | | | | | |
Db 19 CCACCCCAACCCCAACCC 1

RESULT 710

US-10-303-778-1350

; Sequence 1350, Application US/10303778

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL

; FILE REFERENCE: 47416

; CURRENT APPLICATION NUMBER: US/10/303,778

; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1350

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-303-778-1350

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCCACCCCAATCCCTTC 19

RESULT 711

US-10-310-188-48869/c

; Sequence 48869, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FEATURE:
; OTHER INFORMATION: USES THEREOF
FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 48869

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-48869

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1099 ACCCTGGGCTTCAGTCCCG 1117
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ACCCTGGGCTCTCTCCCG 2

RESULT 712

US-10-310-188-59951/c

; Sequence 59951, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 59951

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-59951

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCCTTCCCTACCCCTCC 2

RESULT 713

US-10-310-188-64522

; Sequence 64522, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64522

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-64522

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCAACCCCTTC 1270

Db 1 CCCAGCCCGAGCCCTCC 19
|||||

RESULT 714

US-10-317-277A-67
; Sequence 67, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RFS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-277A-67

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 TTCACCTCCAGCTCCACCT 1150
|||||

Db 1 TTCTTCTGCAGCTCCACCT 19
|||||

RESULT 715

US-10-317-277A-142/c
; Sequence 142, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RFS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-317-277A-142

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1132 TTCACCTCCAGCTCCACCT 1150
|||||

Db 20 TTCTTCTGCAGCTCCACCT 2
|||||

RESULT 716

US-10-349-143-7116/c
; Sequence 7116, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; OTHER INFORMATION: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-24210 for SEQ 3182,
US-10-349-143-7116

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 848 AGATTGAGATGTTAAGG 866
|||||

Db 19 AAATTGAGATGTTAGGG 1
|||||

RESULT 717

US-10-371-474-69
; Sequence 69, Application US/10371474
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
; FILE REFERENCE: RFS-0169
; CURRENT APPLICATION NUMBER: US/10/371,474
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/676,436
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-69

Query Match 0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGCTTTGCC 925
|||||

Db 1 ATTTGTTTCCTCTTTGCC 19
|||||

RESULT 718

US-10-380-126-75/c
; Sequence 75, Application US/10380126
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RFS-0175
; CURRENT APPLICATION NUMBER: US/10/380,126
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/657,042
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA

```

RESULT 720
US-10-483-424-42
; Sequence 42, Application US/10483424
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: ISPH-0692
; CURRENT APPLICATION NUMBER: US/10/483,424
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/912,724
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-483-424-42

```

RESULT 723
US-60-183-791-11958
; Sequence 11958, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 11958

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-11958

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1184 CCGCAGAGAGGTGGACCC 1202
Db      2 CCTGCAGATAGGTGGAACC 20

RESULT 724
US-60-183-791-14782
; Sequence 14782, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14782
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-14782

Query Match      0.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1118 TGCCGAGTCCACCTTCAC 1136
Db      1 TGTCCAATCCAGCTTCAC 19

RESULT 725
US-10-310-188-60224/c
; Sequence 60224, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60224
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-60224

Query Match      0.6%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCCTCC 1248
Db      15 CAGCCCTCGCCTCC 2

RESULT 726
US-10-310-188-9791/c
; Sequence 9791, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9791
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9791

Query Match      0.6%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1089 CTTCCACCCACCC 1102
Db      16 CTTCCACCCACCC 3

RESULT 727
US-09-155-885A-276/c
; Sequence 276, Application US/09155885A
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA: US/09/155,885A
; FILING DATE: 08-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-09-155-885A-276

Query Match      0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5

RESULT 728
US-10-310-188-52565/c
; Sequence 52565, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52565
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-52565

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 876 CTCAGGCACCACAG 889
      |||||||
Db 15 CTCAGGCACCACAG 2

RESULT 729
US-10-453-792-276/c
; Sequence 276, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5

RESULT 730
US-10-606-879-276/c
; Sequence 276, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-606-879-276

Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-453-792-276
```

```
Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 728 GCCAGGAGAAACAG 741
      |||||||
Db 18 GCCAGGAGAAACAG 5
```

```
RESULT 730
US-10-606-879-276/c
; Sequence 276, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 276:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 276:
US-10-606-879-276
```

```
Query Match 0.6%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAG 741
Db 18 GCCAGGAGAAACAG 5

RESULT 731
PCT-US03-05326-389/c
; Sequence 389, Application PC/TUS0305326
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
; TITLE OF INVENTION: Pathways Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/079 (MBHB 02-1105-A)
; CURRENT APPLICATION NUMBER: PCT/US03/05326
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/418,655
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 389
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-05326-389

Query Match 0.8%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 975 GTCCAAGCTCTACT 988
Db 15 GTCCAAGCTCTACT 2

RESULT 732
PCT-US03-05326-568
; Sequence 568, Application PC/TUS0305326
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MYC and MYB Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in the MYC and MYB
; TITLE OF INVENTION: Pathways Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/079 (MBHB 02-1105-A)
; CURRENT APPLICATION NUMBER: PCT/US03/05326
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/418,655
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 568
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05326-568

Query Match 0.6%; Score 14; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 975 GTCCAAGCTCTACT 988
Db 5 GUCCAAGCTCTACT 18

RESULT 733
PCT-US01-17936-12
; Sequence 12, Application PC/TUS0117936
; GENERAL INFORMATION:
; APPLICANT: The Brigham & Women's Hospital, Inc.
; TITLE OF INVENTION: FUSION OF JAZF1 AND JUJAZ1 GENES IN
; TITLE OF INVENTION: ENDOMETRIAL STROMAL TUMORS
; FILE REFERENCE: 05311-024W01
; CURRENT APPLICATION NUMBER: PCT/US01/17936
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
PCT-US01-17936-12

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 CCTCTCTCTTCAAT 945
Db 7 CCTCTCTCTTCAAT 20

RESULT 734
PCT-US03-25389-521/c
; Sequence 521, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Ross, Stuart A
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14

; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 521
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-521

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 17 GAAACAGAACACCG 4
|||||

RESULT 735
PCT-US03-25389-653/c
; Sequence 653, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 653
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-653

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 20 GAAACAGAACACCG 7
|||||

RESULT 736
PCT-US03-25389-1106/c
; Sequence 1106, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-1106

Query Match 0.6%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 18 GAAACAGAACACCG 5
|||||

RESULT 737
PCT-US03-25389-1315/c
; Sequence 1315, Application PC/TUS0325389
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: Antisense Modulation Of Acyl-CoA Synthetase 1 Expression
; FILE REFERENCE: 01294/1/PCT
; CURRENT APPLICATION NUMBER: PCT/US03/25389
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/403,591
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 3624
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1315
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human ACS-1 antisense
PCT-US03-25389-1315

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 GAAACAGAACACCG 748
DB 19 GAAACAGAACACCG 6
|||||

RESULT 738
US-09-874-162A-12
; Sequence 12, Application US/09874162A
; GENERAL INFORMATION:
; APPLICANT: Koontz, Jason
; TITLE OF INVENTION: FUSION OF JAZF1 AND JAZF1 GENES IN
; FILE REFERENCE: 05311-024001
; CURRENT APPLICATION NUMBER: US/09/874,162A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,093
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-874-162A-12

Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 932 CCCTCCTCTTCATT 945
DB 7 CCCTCCTCTTCATT 20
|||||

RESULT 739
US-10-266-090-39932

```
; Sequence 39932, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39932
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-39932
```

```
Query Match 0.6%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1129 ACCTTCACCTCCAG 1142
Db 7 ACCTTCACCTCCAG 20
|||||
```

```
RESULT 740
PCT-US02-16840-2031
; Sequence 2031, Application PC/TUS0216840
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046 (MBHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840-2031
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 821 TGGAGTGCACGAAGTTG 837
Db 1 UGGAGUGGACGAGGUUG 17
|||||
```

```
RESULT 741
PCT-US02-16840-5019/c
; Sequence 5019, Application PC/TUS0216840
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MBHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840-5019
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1112 GTCCCGTGCCCGAGTTCC 1128
Db 17 GTCCACTGCCCGAGTTCC 1
|||||
```

```
RESULT 742
PCT-US02-16840A-2031
; Sequence 2031, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MBHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840A
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840A-2031
```

```
Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 821 TGGAGTGCACGAAGTTG 837
Db 1 UGGAGUGGACGAGGUUG 17
|||||
```

```
RESULT 743
PCT-US02-16840A-5019/c
; Sequence 5019, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/046 (MBHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840A
```

; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-16840A-5019

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCCGAGTTCC 1128
||| |||||
Db 17 GTCCACTGCCAGTTCC 1

RESULT 744

US-09-277-026B-6346
; Sequence 6346, Application US/09277026B
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: Roberts, Elisabeth
; APPLICANT: Jarvis, Thale
; APPLICANT: Coeshott, Claire
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Method and reagents for the treatment of diseases or conditions
; TITLE OF INVENTION: to molecules involved in angiogenic responses
; FILE REFERENCE: MBH00-824-A (239/121)
; CURRENT APPLICATION NUMBER: US/09/277,026B
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/079,678
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 6652
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6346
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-6346

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 4.8e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 787 GAGTGTGTCTCTGTGAG 803
||| :||:|:|:
Db 1 GACUUGUCCUGUAG 17

RESULT 745

US-09-277-026B-6359/c
; Sequence 6359, Application US/09277026B
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: Roberts, Elisabeth
; APPLICANT: Jarvis, Thale
; APPLICANT: Coeshott, Claire
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Method and reagents for the treatment of diseases or conditions
; TITLE OF INVENTION: to molecules involved in angiogenic responses
; FILE REFERENCE: MBH00-824-A (239/121)

; CURRENT APPLICATION NUMBER: US/09/277,026B
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/079,678
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 6652
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Oligonucleotide substrate
US-09-277-026B-6359

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 863 AGGCAGCTGAGACTCA 879
||| |||||
Db 17 AGGAACTGAGACTCA 1

RESULT 746

US-09-572-021-2010/c
; Sequence 2010, Application US/09572021
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McLaughlin, Fiona
; APPLICANT: Randi, Anna Maria
; TITLE OF INVENTION: Method and reagent for the inhibition of ERG
; FILE REFERENCE: 249/006
; CURRENT APPLICATION NUMBER: US/09/572,021
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 5366
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2010
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-572-021-2010

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 752 GCACCTGCCATGACGT 768
||| |||||
Db 17 GCACATGCCATGACGT 1

RESULT 747

US-09-740-332-1266
; Sequence 1266, Application US/09740332
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1266
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1266

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTCACCCACC 1101
||||: |||||
Db 1 CAGGCUCCACCCCAUC 17

RESULT 748

US-09-780-164-840/c
; Sequence 840, Application US/09780164
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 840
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-840

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 TGTGTAACCTCTAAGAA 815
||||: |||||
Db 17 TGTGTAACCTCTAAGAA 1

RESULT 749

US-09-817-879-1266
; Sequence 1266, Application US/09817879
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1266
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1266

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTCACCCACC 1101
||||: |||||
Db 1 CAGGCUCCACCCCAUC 17

RESULT 750

US-09-825-805-676/c
; Sequence 676, Application US/09825805
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 676
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-676

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTGCCAGTTC 1128
||||: |||||
Db 17 GTCCACTGCCAGTTC 1

RESULT 751

US-09-827-395A-328
; Sequence 328, Application US/09827395A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 328
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-328

Query Match 0.6%; Score 13.8; DB 1; Length 17;

Best Local Similarity 76.5%; Pred. No. 4.8e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1045 ACTAAGCCCTGGCCCC 1061
||:|||||:|||||
Db 1 ACUGAGGCCUGGCC 17

RESULT 752
US-09-848-754A-61/c
; Sequence 61, Application US/09848754A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-61

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 860 TTAAGGCACTGAGGAC 876
||:|||||:|||||
Db 17 TTGAGGCAATGAGGAC 1

RESULT 753
US-09-848-754A-2182/c
; Sequence 2182, Application US/09848754A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2182
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-2182

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 859 GTTAAGGCACTGAGGA 875
||:|||||:|||||
Db 17 GTTGAAGGCAATGAGGA 1

RESULT 754
US-09-863-041A-583
; Sequence 583, Application US/09863041A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)

; CURRENT APPLICATION NUMBER: US/09/863,041A
; CURRENT FILING DATE: 2001-05-22
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-863-041A-583

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
||:|||||:|||||
Db 1 CCCCAUCCCAUCCUCC 17

RESULT 755
US-09-864-785-583
; Sequence 583, Application US/09864785
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 583
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-583

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
||:|||||:|||||
Db 1 CCCCAUCCCAUCCUCC 17

RESULT 756
US-10-017-974-8720/c
; Sequence 8720, Application US/10017974
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid-Based Treatment of Diseases or Conditions Related
; FILE OF INVENTION: Nile Virus Infection
; FILE REFERENCE: MBH00,1109-A (400/037)
; CURRENT APPLICATION NUMBER: US/10/017,974
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 37080
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8720
; LENGTH: 17
; TYPE: RNA
; ORGANISM: West Nile virus
US-10-017-974-8720

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Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 995 TTTCTGGGAATCGACA 1011
    ||| ||| ||| ||| |||
Db 17 TTTCTGGGAATCAACA 1

RESULT 757
US-10-156-306-5078/c
; Sequence 5078, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5078
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5078

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1204 CCCTATCAGGGGCTGA 1220
    ||| ||| ||| ||| |||
Db 17 CCATATCAGGGGCTGA 1

RESULT 758
US-10-163-552-364/c
; Sequence 364, Application US/10163552
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; FILE REFERENCE: MBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-364

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCCGAGTCC 1128
    ||| ||| ||| ||| |||
Db 17 GTCCACTCCCGAGTCC 1

RESULT 759
US-10-238-700-3352
; Sequence 3352, Application US/10238700
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBH01-1158-A)
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; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3352
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3352

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 821 TGGAGTCGACGAAGTTG 837
    :|||: |||: |||: |||:
Db 1 UGGAGUGGACGAGGUUG 17

RESULT 760
US-10-294-037A-1194
; Sequence 1194, Application US/10294037A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli O157:H7:EDL933, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,037A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 2772
; SOFTWARE: Proprietary
; SEQ ID NO 1194
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7:EDL933, complete genome.
; FEATURE:
; LOCATION: (1711581)...(1711596)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 1
US-10-294-037A-1194

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 890 TGCTGTTGCCCGCTGTC 906
    ||| ||| ||| ||| |||
Db 1 TGATGTTGCCCGCTGTC 17

RESULT 761
US-10-303-778-3691
; Sequence 3691, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3691
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3691

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCATCCCCCTCCCC 17

RESULT 762

US-10-310-188-5982
; Sequence 5982, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5982
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5982

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 1 CCCCATCCCCCTCCCC 17

RESULT 763

US-10-310-188-7330/c
; Sequence 7330, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7330
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7330

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1169 CCAACTTTCGGCTCCC 1185
Db 17 CCAACTTTCGGCTCCC 1

RESULT 764

US-10-310-188-72805/c
; Sequence 72805, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72805

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72805

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 17 CCCCATCCCCACCCCC 1

RESULT 765

US-10-310-188-72831/c
; Sequence 72831, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72831
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72831

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCAACCCCC 1267
Db 17 CCCCATCCCCACCCCC 1

RESULT 766

US-10-316-954-1929
; Sequence 1929, Application US/10316954
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/316,954
; NUMBER OF SEQ ID NOS: 5998
; SOFTWARE: Proprietary
; SEQ ID NO 1929
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7, complete genome.
; FEATURE:
; LOCATION: (1627606)...(1627622)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-316-954-1929

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 890 TGCTGTCCTGCTGTC 906
Db 1 TGATGTCCTGCTGTC 17

RESULT 767

US-10-430-882-328
; Sequence 328, Application US/10430882


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/ PRIOR FILING DATE: 2001-12-05
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 09/817,879
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 09/740,332
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/611,931
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: US 09/504,321
/ PRIOR FILING DATE: 2000-02-15
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 16207
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3859
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-3859

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.8e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1085 CAGGCTTCACCCACC 1101
Db      |||||:|||||:
1 CAGGCUCCACCCCAUC 17

RESULT 771
US-10-707-147-5148
/ Sequence 5148, Application US/10707147
/ GENERAL INFORMATION:
/ APPLICANT: ROSETTA GENOMICS LTD
/ TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
/ FILE REFERENCE: 49992
/ CURRENT APPLICATION NUMBER: US/10/707,147
/ CURRENT FILING DATE: 2003-11-24
/ NUMBER OF SEQ ID NOS: 20189
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5148
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-707-147-5148

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 752 GCACCTGCCATGCAGGT 768
Db      |||||:|||||:
1 GCACCTGCCGTGCAGGT 17

RESULT 772
US-10-723-361-971
/ Sequence 971, Application US/10723361
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
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/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/ SEQ ID NO 971
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-723-361-971

Query Match      0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CCTGGCCCCAACCCAA 1069
Db      |||||:|||||:
1 CCAGGCCCAAGCCCAA 17

RESULT 773
US-10-723-361-972
/ Sequence 972, Application US/10723361
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
/ FILE REFERENCE: PB0105
/ CURRENT APPLICATION NUMBER: US/10/723,361
/ CURRENT FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: US 09/866,108
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
```

RESULT 774
US-10-724-270-2031
; Sequence 2031, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-972

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1054 CTGGCCCAACCCAG 1070
DB 1 CAGGCCCAAGCCCAAG 17

RESULT 774
US-10-724-270-2031
; Sequence 2031, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2031
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-2031

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 4.8e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 821 TGGAGTGCACGAGTTG 837
DB 1 UGGAGUGGACGAGGUU 17

RESULT 775
US-10-724-270-5019/c
; Sequence 5019, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/046-US (MHB02-326-A)
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5019
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-5019

Query Match 0.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCTGCGCCAGTTC 1128
DB 17 GTCCACTGCCAGTTC 1

RESULT 776
PCT-US03-37416-20
; Sequence 20, Application PC/TUS0337416
; GENERAL INFORMATION:
; APPLICANT: Scios, Inc.
; APPLICANT: Feng, Ying
; APPLICANT: Higgings, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: PCT/US03/37416
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 60/504595
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US03-37416-20

```

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. NO. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1134	CACCTCCAGCTCCACCT	1150
Db	1	CACCTTCAGCGCCACCT	17

RESULT 777
PCT-US96-00362A-67

```

: Sequence 67, Application PC/TUS9600362A
:
: GENERAL INFORMATION:
:
: APPLICANT: Yang, Soo Young
: APPLICANT: Ceréb, Neriá
: TITLE OF INVENTION: Methods and Reagents for Typing HLA
: TITLE OF INVENTION: Class I Genes
: NUMBER OF SEQUENCES: 84
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Opedahl & Larson
: STREET: 1992 Commerce Street Suite 309
: CITY: Yorktown
: STATE: NY
: COUNTRY: US
: ZIP: 10598

```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00362A
;

```

```

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. NO. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 731 AGGAGAAACAGAAACACC 747
Db 2 AGGAGACACGGAAACACC 18

RESULT 778
US-07-999-706-5
; Sequence 5, Application US/07999706
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Regs, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
;

```

; ADDRESS: Dressler, Goldsmith, Shore, Sutter
;
; ADDRESS: Milnamow, Ltd.
; STREET: 180 North Stebson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
;

```

Query Match	0.6%	Score 13.8;	DB 1;	Length 18;
Best Local Similarity	88.2%;	Pred. No. 5.1e+02;		
Matches 15;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY , 1134 CACCTCCAGCTCCACCT 1150
Db 2 CACTTCAGCTCCACAT 18

```

RESULT 779
US-08-170-096-5
; Sequence 5, Application US/08170096
; GENERAL INFORMATION:
; APPLICANT: Denner, Larry A.
; APPLICANT: Rege, Ajay A.
; APPLICANT: Dixon, Richard A.F.
; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY
; NUMBER OF SEQUENCES: 29

```

OTHER INFORMATION: hybridization probe GE2-183 for typing of HLA Class I genes
PCT-US96-00362A-67

```
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/170,096
/ FILING DATE: 20-DEC-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/999,706
/ FILING DATE: December 31, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Katz, Martin L.
/ REGISTRATION NUMBER: 25,011
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)616-5400
/ TELEFAX: (312)616-5460
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-170-096-5

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACTCCAGCTCCACCT 1150
Db 2 CACTCCAGCTCCACAT 18
|||||

RESULT 780
US-09-342-375-67
; Sequence 67, Application US/09342375
; GENERAL INFORMATION:
; APPLICANT: Yang, Soo Young
; APPLICANT: Cereb, Nezh
; TITLE OF INVENTION: Methods and Reagents for Typing HLA
; TITLE OF INVENTION: Class I Genes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: P.O. Box 5270
; CITY: Frisco
; STATE: CO
; COUNTRY: US
; ZIP: 80443
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/342,375
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,081
; FILING DATE: December 22, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: MSK.P-001-DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2082
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
```

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/
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ HYPOTHETICAL: no
/ ANTI-SENSE: yes
/ FRAGMENT TYPE: internal
/ ORIGINAL SOURCE:
/ ORGANISM: human
/ FEATURE:
/ OTHER INFORMATION: hybridization probe GE2-183 for typing of HLA Class I gene:
/ US-09-342-375-67

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AGGAGAAACAGAAACACC 747
Db 2 AGGAGACACGGACACC 18
|||||

RESULT 781
US-09-668-558A-94/c
; Sequence 94, Application US/09668558A
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/09/668,558A
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 94
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide zinc finger nucleotides of SEQID1
/ US-09-668-558A-94

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGAC 1251
Db 17 CAGCCCTCGCTCCAC 1
|||||

RESULT 782
US-09-668-558B-94/c
; Sequence 94, Application US/09668558B
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Fruebis, Joachim
; TITLE OF INVENTION: Methods Of Screening For Compounds That Modulate the
; TITLE OF INVENTION: LSR-Leptin Interaction and Their Use in the Prevention
; TITLE OF INVENTION: and Treatment of Obesity-Related Diseases
; FILE REFERENCE: 70.US2.REG
; CURRENT APPLICATION NUMBER: US/09/668,558B
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,506
; PRIOR FILING DATE: 1999-09-22
```

```

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patent.pm
; SEQ ID NO 94
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide Zinc finger nucleotides of SEQID1
US-09-668-558B-94

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGAC 1251
Db 17 CAGCCCTCGCTCCAC 1

RESULT 783
US-09-703-708-14873
; Sequence 14873, Application US/09703708
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)/C
; CURRENT APPLICATION NUMBER: US/09/703,708
; CURRENT FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/164,320
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/183,791
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-09-703-708-14873

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGAAGTCCAA 980
Db 1 CAATGGTGAAGGCCAA 17

RESULT 784
US-09-969-373-4117/c
; Sequence 4117, Application US/09969373
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)/A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4117
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-4117

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

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Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 912 CTTGGTCTTTGCCCTT 928
Db 18 CTTGGTCTTTGCCCTT 2

RESULT 785
US-10-266-090-50685/c
; Sequence 50685, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50685
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-50685

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
Db 18 CACCACCTCCACCT 2

RESULT 786
US-10-266-090-50690
; Sequence 50690, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50690
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-50690

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
| | | | | | | | | |
Db 1 CACCACCACCTCCACCT 17

RESULT 787

US-10-303-778-5025/c
; Sequence 5025, Application US/10303778

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL

; FILE REFERENCE: 47416

; CURRENT APPLICATION NUMBER: US/10/303,778

; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5025

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-303-778-5025

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1250 ACCCCATCCCAACCCC 1266
| | | | | | | | | |
Db 18 ACCCCACCCCAACCCC 2

RESULT 788

US-10-310-188-6215
; Sequence 6215, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6215

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-6215

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1237 GCCCTGCCTCCGACCC 1253
| | | | | | | | | |
Db 1 GCCCTGCCTCCGACCC 17

RESULT 789

US-10-310-188-9756/c
; Sequence 9756, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9756

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-9756

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1127 CCACCTTCACCTCCAGC 1143
| | | | | | | | | |
Db 17 CCACCTTCACCTCCATC 1

RESULT 790

US-10-310-188-10552/c

; Sequence 10552, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10552

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-10552

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1250 ACCCCATCCCAACCCC 1266
| | | | | | | | | |
Db 18 ACCCCACCCCAACCCC 2

RESULT 791

US-10-310-188-21226

; Sequence 21226, Application US/10310188

; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics

; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G

; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188

; CURRENT FILING DATE: 2002-12-19

; NUMBER OF SEQ ID NOS: 86841

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 21226

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-310-188-21226

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 779 GAGAAACGAGTGTGTC 795
| | | | | | | | | |
Db 1 GAGAAACGAGTGTGTC 17

RESULT 792

US-10-310-188-24811/c

; Sequence 24811, Application US/10310188

; GENERAL INFORMATION:

```
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24811
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-24811

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCCTCGCCTCCGACCC 1254
      |||||
DB 17 CCCTGCCCTCCTACCC 1

RESULT 793
US-10-310-188-25793
; Sequence 25793, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25793
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-25793

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGCTCCACC 1149
      |||||
DB 1 TCTCTCCACCTCCACC 17

RESULT 794
US-10-310-188-30755/c
; Sequence 30755, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30755
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-30755

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAGAAGA 1022
```

```
DB 17 TGGACACCTGCACAAAGA 1
      |||||
RESULT 795
US-10-310-188-34820/c
; Sequence 34820, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34820
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34820

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1120 CCAGTTCACCTTCAC 1136
      |||||
DB 17 CCCAATCCACCTTCAC 1

RESULT 796
US-10-310-188-35499
; Sequence 35499, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35499
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-35499

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1235 CAGCCTCGCCTCCGAC 1251
      |||||
DB 1 CAGCCTCGCGCGCC 17

RESULT 797
US-10-310-188-39123/c
; Sequence 39123, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39123
; LENGTH: 18
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-310-188-39123

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 18 CCCCATCCCCCTCACTCC 2

RESULT 798
US-10-310-188-55156
; Sequence 55156, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55156
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-55156

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 753 CACCTGCCATGCAGTT 769
    ||||| ||||| |||||
Db 1 CACCGCTATGCAGTT 17

RESULT 799
US-10-310-188-60065/c
; Sequence 60065, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60065
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-60065

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 18 CCCCATCCCCCTCACTCC 2

RESULT 800
US-10-310-188-72778/c
; Sequence 72778, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
```

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; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72778
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72778

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 17 CCCCATCCCCCACTCC 1

RESULT 801
US-10-310-188-72795/c
; Sequence 72795, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72795
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72795

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCCAACCCCT 1267
    ||||| ||||| |||||
Db 17 CCCCATCCCCCACTCC 1

RESULT 802
US-10-310-188-72796/c
; Sequence 72796, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72796
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72796

Query Match          0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1252 CCCATCCCCCAACCCCT 1268
    ||||| ||||| |||||
Db 18 CCCATCCCCCACTCC 2
```

```
RESULT 803
US-10-310-188-72799/c
; Sequence 72799, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72799
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72799

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCACCCCC 1267
Db 18 CCCACCCCCACCCCC 2

RESULT 804
US-10-310-188-85927/c
; Sequence 85927, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85927
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85927

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 TTTTATCCCTCTCTTC 942
Db 18 TCTTATTCCTCTCTTC 2

RESULT 805
US-10-718-948-20
; Sequence 20, Application US/10718948
; GENERAL INFORMATION:
; APPLICANT: Feng, Ying
; APPLICANT: Higgins, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: US/10/718,948
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/504585
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
```

```
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-718-948-20

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
Db 1 CACCTTCAGGCCACCT 17

RESULT 806
US-60-164-320-14873
; Sequence 14873, Application US/60164320
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)A
; CURRENT APPLICATION NUMBER: US/60/164,320
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-164-320-14873

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGGAGTCCAA 980
Db 1 CAATGGTGGAGGCCAA 17

RESULT 807
US-60-183-791-14873
; Sequence 14873, Application US/60183791
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15804)B
; CURRENT APPLICATION NUMBER: US/60/183,791
; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 14873
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-14873

Query Match      0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 964 CAACGGTGGAGTCCAA 980
Db 1 CAATGGTGGAGGCCAA 17

RESULT 808
US-10-321-039-630
```

; Sequence 630, Application US/10321039
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 630
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-630

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GCCACAGAGCCTGAGCA 1312
|||||
DB 2 GCCACAGAGCCTGGAGA 18

RESULT 809
US-10-354-953-757
; Sequence 757, Application US/10354953
; GENERAL INFORMATION:
; APPLICANT: Dorn, Erin
; APPLICANT: Rasmussen, Eric
; TITLE OF INVENTION: Pharmacogenetic DME Detection Assay Methods and Kits
; FILE REFERENCE: FORS-07810
; CURRENT APPLICATION NUMBER: US/10/354,953
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 1120
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 757
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-354-953-757

Query Match 0.6%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GCCACAGAGCCTGAGCA 1312
|||||
DB 2 GCCACAGAGCCTGGAGA 18

RESULT 810
PCT-US00-13327-46/c
; Sequence 46, Application PC/TUS0013327
; GENERAL INFORMATION:
; APPLICANT: McGrail, Maura
; APPLICANT: Russell, Deanna L.
; APPLICANT: Shattuck, Donna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: DIABETES GENE

; FILE REFERENCE: Diabetes Gene III
; CURRENT APPLICATION NUMBER: PCT/US00/13327
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: US 60/174,700
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/135,423
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-13327-46

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
|||||
DB 19 CACCTTGAGAGTGGG 3

RESULT 811
PCT-US00-13327-48/c
; Sequence 48, Application PC/TUS0013327
; GENERAL INFORMATION:
; APPLICANT: McGrail, Maura
; APPLICANT: Russell, Deanna L.
; APPLICANT: Shattuck, Donna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: DIABETES GENE
; FILE REFERENCE: Diabetes Gene III
; CURRENT APPLICATION NUMBER: PCT/US00/13327
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: US 60/174,700
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/135,423
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-13327-48

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
|||||
DB 19 CACCTTGAGAGTGGG 3

RESULT 812
PCT-US02-25943-36695
; Sequence 36695, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 36695
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:

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; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 39327
PCT-US02-25943-36695

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1087 GGCTTACCCGCCCT 1103
Db 2 GGCTTACCCGCCCT 18

RESULT 813
PCT-US03-05045-87/c
; Sequence 87, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sina sense
PCT-US03-05045-87

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCCGTCC 1128
Db 19 GTCCCGTCCCGTCC 3

RESULT 814
PCT-US03-05045-90/c
; Sequence 90, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
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; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/sina sense
PCT-US03-05045-90

Query Match
Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 739 CAGACACCGTGTGCAC 755
Db 17 CAGACACCGTGTGCAC 1

RESULT 815
PCT-US03-05045-336
; Sequence 336, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MBHB 02-468-B)
; CURRENT APPLICATION NUMBER: PCT/US03/05045
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
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; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 336
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05045-336

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTGGCCAGTTCC 1128
      ||| :|||||:|
Db 1 GUCCACUGCCAGUCC 17

RESULT 816
PCT-US03-05045-339
; Sequence 339, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MHBB 02-468-B)
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US03/05045
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 339
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05045-339

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTGGCCAGTTCC 1128
      ||| :|||||:|
Db 1 GUCCACUGCCAGUCC 17

RESULT 816
PCT-US03-05045-339
; Sequence 339, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MHBB 02-468-B)
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US03/05045
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/277,494
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 339
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05045-339
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05045-339

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 5.3e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 739 CAGAACACCGTGTGCAC 755
      ||| :|||||:|
Db 3 CAGGCGACCGUGGCAC 19

RESULT 817
PCT-US03-05045-524/c
; Sequence 524, Application PC/TUS0305045
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Jamison, Sharon
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 400/081 (MHBB 02-468-B)
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: PCT/US03/05045
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/251,117
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1263
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 524
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sens
PCT-US03-05045-524

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 858 TGTTAAGGGCACTGAGG 874
      ||| :|||||:|
Db 17 TGTTGAGGGCAATGAGG 1

RESULT 818
PCT-US03-05045-831
; Sequence 831, Application PC/TUS0305045
; GENERAL INFORMATION:
```

APPLICANT: Sinna Therapeutics Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
APPLICANT: Fosnaugh, Kathy
APPLICANT: Jamison, Sharon
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
FILE REFERENCE: 400/081 (WBHB 02-468-B)
CURRENT APPLICATION NUMBER: PCT/US03/05045
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 10/251,117
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 10/163,552
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 10/277,494
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 09/916,466
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1263
SOFTWARE: PatentIn version 3.2
SEQ ID NO 831
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
PCT-US03-05045-831

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 858 TGTTAAGGCACTGAGG 874
Db 3 UGUUGAGGCAUGAGG 19

RESULT 819
US-09-573-425-46/c
Sequence 46, Application US/09573425
GENERAL INFORMATION:
APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shattuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: US 60/135,423
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens

US-09-573-425-46

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
Db 19 CACCCCTTGAGAAGTGGG 3

RESULT 820
US-09-573-425-48/c
Sequence 48, Application US/09573425
GENERAL INFORMATION:
APPLICANT: McGrail, Maura
APPLICANT: Russell, Deanna L.
APPLICANT: Shattuck, Donna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: DIABETES GENE
FILE REFERENCE: Diabetes Gene III
CURRENT APPLICATION NUMBER: US/09/573,425
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/174,700
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: US 60/135,423
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-573-425-48

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1263 CCCCTTCAGAGTGGG 1279
Db 19 CACCCCTTGAGAAGTGGG 3

RESULT 821
US-10-016-490C-24/c
Sequence 24, Application US/10016490C
GENERAL INFORMATION:
APPLICANT: Yin, James Q.
TITLE OF INVENTION: Methods for design and selection of short double-stranded
oligonucleotides, and compounds of gene drugs
FILE REFERENCE: 01-2793
CURRENT APPLICATION NUMBER: US/10/016,490C
CURRENT FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: The same as those in human.
US-10-016-490C-24

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 TTGAGTCCCGTGCCAG 1124
Db 17 TTCAGTTCCTGTCACAG 1

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RESULT 822
US-10-227-565-36695
; Sequence 36695, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 36695
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 39327
US-10-227-565-36695

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1087 GGCTTACCCACCCT 1103
||||| | |||||
Db 2 GGCTTACGCCACCCT 18

RESULT 823
US-10-251-117-87/c
; Sequence 87, Application US/10251117
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-251-117-87

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCAGTTC 1128
||||| | |||||
Db 19 GTCCACTGCCAGTTC 3

RESULT 824
US-10-251-117-90/c
; Sequence 90, Application US/10251117
; GENERAL INFORMATION:
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-90

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 739 CAGAACACCGTGTGCAC 755
||||| | |||||
Db 17 CAGGCACCGTGTGCAC 1

RESULT 825
US-10-251-117-336
; Sequence 336, Application US/10251117
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-336

Query Match          0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1112 GTCCCGTCCAGTTC 1128
||||| | |||||
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Db 1 GUCCACUGCCAGUCC 17

RESULT 826

US-10-251-117-339

Sequence 339, Application US/10251117

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor Receptor

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (MEHB02-468-A)

CURRENT APPLICATION NUMBER: US/10/251,117

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 10/163,552

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 09/916,466

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: US 60/296,249

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE: PatentIn version 3.0

SEQ ID NO 339

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-251-117-339

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;

Mismatches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 739 CAGACACCGGTGTGCAC 755

Db 3 CAGGCGACCGUGGCAC 19

RESULT 827

US-10-251-117-578/c

Sequence 578, Application US/10251117

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor Receptor

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (MEHB02-468-A)

CURRENT APPLICATION NUMBER: US/10/251,117

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 10/163,552

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 09/916,466

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: US 60/296,249

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE: PatentIn version 3.0

SEQ ID NO 578

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense

US-10-251-117-578

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 858 TGTTAAGGCGCACTGAGG 874

Db 17 TGTGAGGCGCAATGAGG 1

RESULT 828

US-10-251-117-885

Sequence 885, Application US/10251117

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor Receptor

TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

FILE REFERENCE: 900/042 (MEHB02-468-A)

CURRENT APPLICATION NUMBER: US/10/251,117

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/393,924

PRIOR FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 10/163,552

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 09/916,466

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: US 60/296,249

PRIOR FILING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 1213

SOFTWARE: PatentIn version 3.0

SEQ ID NO 885

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-251-117-885

Query Match

Best Local Similarity 0.6%; Score 13.8; DB 1; Length 19;

Mismatches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 858 TGTTAAGGCGCACTGAGG 874

Db 3 UGUUGAGGCGCAUAGG 19

RESULT 829

US-10-266-090-46529/c

Sequence 46529, Application US/10266090

GENERAL INFORMATION:

APPLICANT: GOFF, STEPHEN

APPLICANT: BONAN, CAROLINE

APPLICANT: COLBERT, MICHELLE

APPLICANT: WANG, RONG-LIN

TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES

FILE REFERENCE: NADII.058C1

CURRENT APPLICATION NUMBER: US/10/266,090

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: US 10/260,703

PRIOR FILING DATE: 2002-09-26

PRIOR APPLICATION NUMBER: US 60/326,117

PRIOR FILING DATE: 2001-09-26

NUMBER OF SEQ ID NOS: 51812

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 46529

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-46529

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCACCT 1150
      |||||
Db 19 CTCCTCCAGCTCCAACT 3

RESULT 830
US-10-293-338-6274
; Sequence 6274, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6274
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-6274

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 750 GTGCACCTGCCATGCAG 766
      |||||
Db 1 GTGCGCTGCCAGGCAG 17

RESULT 831
US-10-303-778-12689
; Sequence 12689, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12689
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-12689

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 918 TCTTTCCTTTTATCCC 934
      |||||
Db 2 TCTTTCCTTTTATCCC 18

RESULT 832
US-10-310-188-1678/c
; Sequence 1678, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENH
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1678
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-1678

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1244 CCTCCGACCCCATCCC 1260
      |||||
Db 17 CCTCAGACACCATCCC 1

RESULT 833
US-10-310-188-6272
; Sequence 6272, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6272
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-6272

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1099 ACCCTGGCTTCAGTCC 1115
      |||||
Db 2 ACCCTGGCTTCAGGCC 18

RESULT 834
US-10-310-188-10574/c
; Sequence 10574, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10574
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-10574

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1243 GCCTCCGACCCCATCCC 1259
      |||||
Db 18 GCCTCCGACCCCATCCC 2
```

```
RESULT 835
US-10-310-188-18123/c
; Sequence 18123, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18123
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18123

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1245 CTCGACCCCATCCCA 1261
    ||||| ||||| |||||
Db 17 CTCGACCCCATCCCA 1

RESULT 836
US-10-310-188-23028
; Sequence 23028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23028
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23028

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 918 TCCTTTCCTTTTATCCC 934
    ||||| ||||| |||||
Db 2 TCCTTTCCTTTTATCCC 18

RESULT 837
US-10-310-188-33554
; Sequence 33554, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33554
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-33554

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 918 TCCTTTCCTTTTATCCC 934
    ||||| ||||| |||||
Db 2 TCCTTTCCTTTTATCCC 18
```

```
Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 CACCTGAAAAAGAGGG 1026
    ||||| ||||| |||||
Db 1 CCACTGAAAAAGAGAGG 17

RESULT 838
US-10-310-188-34905/c
; Sequence 34905, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34905
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34905

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1120 CCCATTCCACCTTCAC 1136
    ||||| ||||| |||||
Db 17 CCCATTCCACCTTCAC 1

RESULT 839
US-10-310-188-72813/c
; Sequence 72813, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72813
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72813

Query Match      0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCACCCCC 1267
    ||||| ||||| |||||
Db 17 CCCCATCCCCACCCCC 1

RESULT 840
US-10-310-188-72814/c
; Sequence 72814, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```

; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72814
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72814

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1251 CCCCATCCCCACCCCC 1267
| | | | | | | | | | | | | | | | | | | | |
Db 18 CCCACCCCCCCCCC 2

RESULT 841

US-10-310-188-75577/c
; Sequence 75577, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75577
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-75577

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1239 CCTCGCTCGGACCCCA 1255
| | | | | | | | | | | | | | | | | | | | |
Db 19 CTTGCGCTCGGCCCCA 3

RESULT 842

US-10-310-188-78419/c
; Sequence 78419, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78419
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-78419

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1254 CATCCCCACCCCTTC 1270
| | | | | | | | | | | | | | | | | | | | |
Db 19 CCTCCCCACCCCTTC 3

RESULT 843

US-10-367-832A-36695
; Sequence 36695, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 36695
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3597227)...(3597245)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 392
US-10-367-832A-36695

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1087 GGCCTTCACTCCACCCCT 1103
| | | | | | | | | | | | | | | | | | | | |
Db 2 GGCCTTCACTCCACCCCT 18

RESULT 844

US-60-216-745-8300/c
; Sequence 8300, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaire-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
; FILE REFERENCE: 84 US1,PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pn
; SEQ ID NO 8300
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-54711 for SEQ 3769,
US-60-216-745-8300

Query Match 0.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 802 AGTAACAGTAAAGAAAG 818
| | | | | | | | | | | | | | | | | | | | |
Db 18 AGTAACAGTAAAGAAAG 2

RESULT 845

US-08-729-043-2
; Sequence 2, Application US/08729043
; GENERAL INFORMATION:
; APPLICANT: Leushner, James
; TITLE OF INVENTION: Method, Composition and Kit for Typing
; TITLE OF INVENTION: Classical HLA Class I Genes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street Suite 309

CITY: Yorktown
STATE: NY
COUNTRY: US
ZIP: 10598
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: VGEN.P-037-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE: human
ORGANISM: human
FEATURE:
OTHER INFORMATION: amplification primer for exons 2 and 3 of
US-08-729-043-2

Query Match 0.6%; Score 13.6; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2042 GCCCTCTGCTGACACGA 2061
Db 1 GCCCTCTGCGGGAAGCA 20

RESULT 846
PCT-US02-25944-7396
Sequence 7396, Application PC/TUS0225944
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25944
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7396
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (15497)...(15511)
OTHER INFORMATION: Chromosome =11 Strand = negative ConnectronObjectNumber = 8924
PCT-US02-25944-7396

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
Db 1 TGTTCATTTTCTTTG 15

RESULT 847
PCT-US02-25944-7448
Sequence 7448, Application PC/TUS0225944
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25944
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7448
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (641065)...(641079)
OTHER INFORMATION: Chromosome =13 Strand = positive ConnectronObjectNumber = 111
PCT-US02-25944-7448

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
Db 1 TGTTCATTTTCTTTG 15

RESULT 848
US-10-227-564-7396
Sequence 7396, Application US/10227564
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,564
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 9208
SOFTWARE: Proprietary
SEQ ID NO 7396
LENGTH: 15
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.
FEATURE:
LOCATION: (15497)...(15511)
OTHER INFORMATION: Chromosome =11 Strand = negative ConnectronObjectNumber = 8;
US-10-227-564-7396

Query Match 0.6%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 902 TGGTCATTTTCTTTG 916
Db 1 TGTTCATTTTCTTTG 15

RESULT 849
US-10-227-564-7448
Sequence 7448, Application US/10227564
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,564
CURRENT FILING DATE: 2002-08-26

```

; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7448
; LENGTH: 15

```

TYPE: DNA
ORGANISM: Saccharomyces cerevisiae complete genome.

Query Match	0.6%	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%	Pred. No. 4.8e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Query Match	0.6%	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%;	Pred. No. 4.8e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Query Match	0.6%	Score 13.4;	DB 1;	Length 15;
Best Local Similarity	93.3%	Pred. No. 4.8e+02;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1097 CCACCCCTGGGCTTCA 1111
Db 15 CCGCCCTGGGCTTCA 1

```

Query Match          0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

SEQ ID NO 10
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-573-684-10

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1184 CCGCAGAGAGGTGG 1198
||||| |||||
Db 15 CCGCGCAGAGGTGG 1

RESULT 855
US-10-227-563-3485
Sequence 3485, Application US/10227563
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,563
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 3485
LENGTH: 16
TYPE: DNA
ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
FEATURE:
LOCATION: (437846)...(437861)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4094

US-10-227-563-3485

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCCTCCG 1249
||||| |||||
Db 1 CAGCCCTCGCCTCCG 15

RESULT 856
US-10-294-040-85/c
Sequence 85, Application US/10294040
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,040
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: Proprietary
SEQ ID NO 85
LENGTH: 16
TYPE: DNA
ORGANISM: Helicobacter pylori 26695 complete genome.
FEATURE:
LOCATION: (137511)...(137526)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 135

US-10-294-040-85

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCCTTGGCTT 921
||||| |||||
Db 15 ATTTCCTTGGCTT 1

RESULT 857

US-10-310-188-78695/c
Sequence 78695, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics

TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 47497
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78695
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-78695

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1244 CCTCCGACCCCATCC 1258
||||| |||||
Db 15 CCTCCGACCCCATCC 1

RESULT 858

US-10-367-892-3485
Sequence 3485, Application US/10367892
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.

TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,892
CURRENT FILING DATE: 2003-03-06
NUMBER OF SEQ ID NOS: 25502
SOFTWARE: Proprietary
SEQ ID NO 3485
LENGTH: 16
TYPE: DNA
ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
FEATURE:
LOCATION: (437846)...(437861)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4

US-10-367-892-3485

Query Match 0.6%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCCTCCG 1249
||||| |||||
Db 1 CAGCCCTCGCCTCCG 15

RESULT 859

US-10-659-948A-10/c
Sequence 10, Application US/10659948A
GENERAL INFORMATION:
APPLICANT: Hovav, Timothy A

TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659,948A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,218
PRIOR FILING DATE: 2002-09-19


```
QY 907 ATTCTTTGGTCTT 921
|:::|:::|:::|
Db 3 AUUUUUUUUGUUU 17

RESULT 864
US-09-531-025A-1602
; Sequence 1602, Application US/09531025A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH800-845-E (247/277)
; CURRENT APPLICATION NUMBER: US/09/531,025A
; CURRENT FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-531-025A-1602

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTT 923
|:::|:::|:::|
Db 1 UUUUUUUUGUUU 15

RESULT 865
US-09-541-946-1657/c
; Sequence 1657, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altschuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1657
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1657

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTT 923
|:::|:::|:::|
Db 1 UUUUUUUUGUUU 15

RESULT 866
US-09-541-946-1659/c
; Sequence 1659, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altschuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1659

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTT 923
|:::|:::|:::|
Db 1 UUUUUUUUGUUU 15

RESULT 867
US-09-546-745A-6637
; Sequence 6637, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6637
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-6637

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1073 TCAGTCCCACTCCAG 1087
|:::|:::|:::|
Db 15 TGAGTCCCACTCCAG 1

RESULT 866
US-09-541-946-1659/c
; Sequence 1659, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altschuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,248
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1659

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1073 TCAGTCCCACTCCAG 1087
|:::|:::|:::|
Db 15 TGAGTCCCACTCCAG 1

RESULT 867
US-09-546-745A-6637
; Sequence 6637, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6637
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-6637

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1065 CCCAGCTTCAGTCC 1079
Db 1 CCCAGCTTCAGTCC 15
|||||:|:|:|

RESULT 868
US-09-572-021-1505/C
; Sequence 1505, Application US/09572021
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McLaughlin, Fiona
; APPLICANT: Randi, Anna Maria
; TITLE OF INVENTION: Method and Reagent for the Inhibition of ERG
; FILE REFERENCE: 249/006
; CURRENT APPLICATION NUMBER: US/09/572,021
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 5366
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-572-021-1505

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 752 GCACCTGCCATGCAG 766
Db 16 GCACATGCCATGCAG 2
|||||:|:|:|

RESULT 869
US-09-636-385-909
; Sequence 909, Application US/09636385
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-F (250/125)
; CURRENT APPLICATION NUMBER: US/09/636,385
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 09/436,430
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-636-385-909

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGCTCTT 921
|:|:|:|:|:|:|:|:|

Db 3 AUUUUUUUUGUUU 17

RESULT 870
US-09-636-385-1602
; Sequence 1602, Application US/09636385
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-F (250/125)
; CURRENT APPLICATION NUMBER: US/09/636,385
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6341
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-636-385-1602

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGCTCTT 923
|:|:|:|:|:|:|:|:|

Db 1 UUUUUUUUGUUU 15

RESULT 871
US-09-696-347-909
; Sequence 909, Application US/09696347
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/001
; CURRENT APPLICATION NUMBER: US/09/696,347
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6389
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA

```
; ORGANISM: Hepatitis B Virus
US-09-696-347-903

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTCTTTGCTTGT 921
Db 3 AUUUCUUUGUUU 17

RESULT 872
US-09-696-347-1602
; Sequence 1602, Application US/09696347
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Ken
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/001
; CURRENT APPLICATION NUMBER: US/09/696,347
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 07/982,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6389
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-09-696-347-1602

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGCTTGT 923
Db 1 UUUUUUUUGUUU 15

RESULT 873
US-09-780-533A-1806/c
; Sequence 1806, Application US/09780533A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
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```
; SEQ ID NO 1806
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1806

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1135 ACCTCCAGCTCCAC 1149
Db 17 ACCTCCAGCTCCCTC 3

RESULT 874
US-09-780-533A-2377/c
; Sequence 2377, Application US/09780533A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2377
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2377

Query Match
Best Local Similarity 0.6%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1134 CACCTCCAGCTCCAC 1148
Db 15 CACCTCCAGCTCCTC 1

RESULT 875
US-09-818-875-559/c
; Sequence 559, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-818-875-559

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||
Db 15 TGTATCGCTACCAAC 1

RESULT 876

US-09-818-875-560
; Sequence 560, Application US/09818875
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-560

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||
Db 3 TGTATCGCTACCAAC 17

RESULT 877

US-09-877-478-909
; Sequence 909, Application US/09877478
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1602

; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-909

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
|:::|:::|:::
Db 3 AUUUCUUUGUCUU 17

RESULT 878

US-09-877-478-1602
; Sequence 1602, Application US/09877478
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-1602

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTTG 923
|:::|:::|:::
Db 1 UUUUUUUUGUCUU 15

RESULT 879

US-10-060-830-203
; Sequence 203, Application US/10060830
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong

;; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
;; FILE REFERENCE: PB0169
;; CURRENT APPLICATION NUMBER: US/10/060,830
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/325,062
;; PRIOR FILING DATE: 2001-09-25
;; NUMBER OF SEQ ID NOS: 1123
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 203
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-830-203

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 879 AGGCACACAGTGCT 893
|||
DB 3 AGTCACACAGTGCT 17

RESULT 880
US-10-060-830-206
;; Sequence 206, Application US/10060830
;; GENERAL INFORMATION:
;; APPLICANT: Nguyen, Hung-Tuong
;; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
;; FILE REFERENCE: PB0169
;; CURRENT APPLICATION NUMBER: US/10/060,830
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/325,062
;; PRIOR FILING DATE: 2001-09-25
;; NUMBER OF SEQ ID NOS: 1123
;; SOFTWARE: Acomica Sequence Listing Engine
;; SEQ ID NO 206
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-830-206

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 880 GGCACACAGTGCTG 894
|||
DB 1 GTCACACAGTGCTG 15

RESULT 881
US-10-209-787-559/C
;; Sequence 559, Application US/10209787
;; GENERAL INFORMATION:
;; APPLICANT: Kmiec, Eric B.
;; APPLICANT: Gamper, Howard B.
;; APPLICANT: Rice, Michael C.
;; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
;; TITLE OF INVENTION: Stranded Oligonucleotides
;; FILE REFERENCE: Napro-4
;; CURRENT APPLICATION NUMBER: US/10/209,787
;; CURRENT FILING DATE: 2002-07-30
;; PRIOR APPLICATION NUMBER: US 09/818,875
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,176
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,179
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/208,538
;; PRIOR FILING DATE: 2000-06-01
;; PRIOR APPLICATION NUMBER: US 60/244,989
;; PRIOR FILING DATE: 2000-10-30
;; NUMBER OF SEQ ID NOS: 4385
;; SOFTWARE: Friedman macro Napro4
;; SEQ ID NO 559
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-209-787-559

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||
DB 15 TGTATCGCTACCAAC 1

RESULT 882
US-10-209-787-560
;; Sequence 560, Application US/10209787
;; GENERAL INFORMATION:
;; APPLICANT: Kmiec, Eric B.
;; APPLICANT: Gamper, Howard B.
;; APPLICANT: Rice, Michael C.
;; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
;; TITLE OF INVENTION: Stranded Oligonucleotides
;; FILE REFERENCE: Napro-4
;; CURRENT APPLICATION NUMBER: US/10/209,787
;; CURRENT FILING DATE: 2002-07-30
;; PRIOR APPLICATION NUMBER: US 09/818,875
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,176
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/192,179
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US 60/208,538
;; PRIOR FILING DATE: 2000-06-01
;; PRIOR APPLICATION NUMBER: US 60/244,989
;; PRIOR FILING DATE: 2000-10-30
;; NUMBER OF SEQ ID NOS: 4385
;; SOFTWARE: Friedman macro Napro4
;; SEQ ID NO 560
;; LENGTH: 17
;; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-10-209-787-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17

RESULT 883
US-10-261-185-559/c
; Sequence 559, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-559

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1

RESULT 884
US-10-261-185-560
; Sequence 560, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
```

```
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17

RESULT 885
US-10-310-188-37271
; Sequence 37271, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GI
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37271
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-37271

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 865 GGCACCTGAGGACTCA 879
Db 2 GGCCTGTGAGGACTCA 16

RESULT 886
US-10-339-782-328
; Sequence 328, Application US/10339782
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-0001100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 328
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-328

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1091 TCACCCCCCACCCTGG 1105
Db 3 TCAGCCCCCACCCTGG 17

RESULT 887
```

```
US-10-342-902-909
; Sequence 909, Application US/10342902
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-909

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCCTTGGCTT 921
Db 3 AOUUCUUUGUCUU 17
|:::|:::|:::|:::|

RESULT 888
US-10-342-902-1602
; Sequence 1602, Application US/10342902
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1602
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```
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-1602

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTTCTTTGGTCTTTG 923
Db 1 UUUUUUUUGUCUUUG 15
|:::|:::|:::|:::|

RESULT 889
US-10-623-107-559/c
; Sequence 559, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEIC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: NAPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-559

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1
|:::|:::|:::|:::|

RESULT 890
US-10-623-107-560
; Sequence 560, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEIC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: NAPRO-14 US
; CURRENT APPLICATION NUMBER: US/10/623,107
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-560

Query Match          0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 3 TGTATCGCTACCAAC 17
|:::|:::|:::|:::|

RESULT 891
```

```
US-10-669-841-909
; Sequence 909, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-B)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 909
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-909

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGCTT 921
Db 3 AUUUUUUUUUUUUUU 17

RESULT 892
US-10-669-841-1602
; Sequence 1602, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-B)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
```

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US-10-669-841-1602
; Sequence 909, Application US/10669841
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-B)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1602
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-1602

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 26.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTTTGGCTTTG 923
Db 1 UUUUUUUUUUUUU 15

RESULT 893
US-10-681-074-559/c
; Sequence 559, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: Napro-18 US
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-559

Query Match      0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
Db 15 TGTATCGCTACCAAC 1

RESULT 894
US-10-681-074-560
; Sequence 560, Application US/10681074
```

GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; FILE REFERENCE: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US/10/681,074
; PRIOR FILING DATE: 2003-10-07
; PRIOR FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-560

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 953 TGTATCGCTACCAAC 967
|||||||
Db 3 TGTATCGCTACCAAC 17

RESULT 895
US-10-723-361-973
; Sequence 973, Application US/10723361
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 973
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-973

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1056 GGCCCCAACCCCAAG 1070
|||||||
Db 2 GGCCCCAACCCCAAG 16

RESULT 896
US-10-723-361-974
; Sequence 974, Application US/10723361
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 974
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-974

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1056 GGCCCCAACCCCAAG 1070
|||||||
Db 1 GGCCCCAACCCCAAG 15

RESULT 897
US-10-741-600-73370/c
; Sequence 73370, Application US/10741600
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73370
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73370

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGCTCCA 1147
| | | | | | | | | | | | | | | | | | | | | |
Db 15 TCACCTGCAGCTCCA 1

RESULT 898
US-60-325-062-203
; Sequence 203, Application US/60325062
; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
; FILE REFERENCE: AROMICA-22
; CURRENT APPLICATION NUMBER: US/60/325,062
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aromica Sequence Listing Engine
; SEQ ID NO 203
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-325-062-203

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 879 AGGCACACAGTGCT 893
| | | | | | | | | | | | | | | | | | | | | |
Db 3 AGTCACACAGTGCT 17

RESULT 899
US-60-325-062-206
; Sequence 206, Application US/60325062
; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL_DOMAN CONTAINING PROTEIN
; FILE REFERENCE: AROMICA-22
; CURRENT APPLICATION NUMBER: US/60/325,062
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aromica Sequence Listing Engine
; SEQ ID NO 206
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-325-062-206

Query Match 0.6%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 880 GGCACACAGTGCTG 894
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTCACACAGTGCTG 15

RESULT 900
PCT-US02-00985-19/c
; Sequence 19, Application PC/TUS0200985
; GENERAL INFORMATION:

; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; TITLE OF INVENTION: NANOPARTICLES CONTAINING POLYMERIC NUCLEIC ACID HOMOLOGS,
; TITLE OF INVENTION: PHARMACEUTICAL....
; FILE REFERENCE: 325/87
; CURRENT APPLICATION NUMBER: PCT/US02/00985
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/335,837
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
PCT-US02-00985-19

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCTGGGCTTC 1110
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CCCACATGGGCTTC 3

RESULT 901
PCT-US02-24115-32/c
; Sequence 32, Application PC/TUS0224115
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TOLAND, Amanda E.
; APPLICANT: BALMAIN, Allan
; TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANC
; FILE REFERENCE: UCSE1120-2MO
; CURRENT APPLICATION NUMBER: PCT/US02/24115
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/334,146
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/308,911
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Amplification reaction primer
PCT-US02-24115-32

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1093 ACCCCACCTGGGC 1107
Db 15 ACCCTCACCTGGGC 1

RESULT 902
PCT-US02-25940-18207
; Sequence 18207, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
PCT-US02-25940-18207

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1055 TGGCCCCCAACCCAA 1069
Db 4 TGGCCCCCAACCCAA 18

RESULT 903
PCT-US02-34679-162/c
; Sequence 162, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Vellicelebi, Gonul
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
```

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; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-162

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 812 AGAAAAGCCTGGAGT 826
Db 16 AGAGAGCCTGGAGT 2

RESULT 904
PCT-US03-07585-40
; Sequence 40, Application PC/TUS0307585
; GENERAL INFORMATION:
; APPLICANT: Holland-Staley, Carol
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: IDENTIFYING AND CHARACTERIZING HEPATITIS C
; FILE REFERENCE: PCV-001PC
; CURRENT APPLICATION NUMBER: PCT/US03/07585
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,603
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US03-07585-40

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1056 GGCCCCCAACCCAAAG 1070
Db 4 GGCCCCCAACCCAAAG 18

RESULT 905
PCT-US02-00985-19/c
; Sequence 19, Application PC/TIL0200985
; GENERAL INFORMATION:
; APPLICANT: Yissum Research Development Company of The Hebrew University of Jerusalem
; TITLE OF INVENTION: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW UNIVERSITY OF JERUSALEM
; TITLE OF INVENTION: NANOPARTICLES CONTAINING POLYMERIC NUCLEIC ACID HOMOLOGS,
; FILE REFERENCE: 325/87
; CURRENT APPLICATION NUMBER: PCT/IL02/00985
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/335,837
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Mus musculus
```

PCT-IL02-00985-19

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCACCTGGGCTTC 1110
|||||
Db 17 CCACCATGGGCTTC 3

RESULT 906

US-09-155-885A-270/c

; Sequence 270, Application US/09155885A

; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN

; ROSSAU, RUDI

; MAERTENS, GEERT

; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/155.885A

; FILING DATE: 08-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP97/02002

; FILING DATE: 21-APR-1997

; APPLICATION NUMBER: EP 96870053.4

; FILING DATE: 19-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.

; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 2551-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 270:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 270:

US-09-155-885A-270

Query Match

0.6%; Score 13.4; DB 1; Length 18;

Best Local Similarity 93.3%; Pred. No. 5.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742

|||||

Db 18 GCCAAGAGAAACAGA 4

RESULT 907

US-09-155-885A-272/c

; Sequence 272, Application US/09155885A

; GENERAL INFORMATION:

APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 272:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-09-155-885A-272
Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 728 GCCAGGAGAAACAGA 742
|||||
Db 18 GCCATGAGAAACAGA 4
RESULT 908
US-09-155-885A-273/c
; Sequence 273, Application US/09155885A
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-155-885A-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACGGA 4

RESULT 909
US-09-857-278-18
Sequence 18, Application US/09857278
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
FILE REFERENCE: RTSP-0142
CURRENT APPLICATION NUMBER: US/09/857,278
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/205,204
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 18
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-857-278-18

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 761 ATGCAGGTTTCTTC 775
Db 4 ATGCAGGTTTCTTC 18

RESULT 910
US-10-108-732-47/c

Sequence 47, Application US/10108732
GENERAL INFORMATION:
APPLICANT: Box, Neil F
APPLICANT: Duffy, David L
APPLICANT: Hayward, Nicholas K
APPLICANT: Martin, Nicholas G
APPLICANT: Sturm, Richard A
APPLICANT: Gruis, Nelske A
APPLICANT: Van Der Velden, Pieter
APPLICANT: Bergman, Wilma
APPLICANT: Frants, Rune R
TITLE OF INVENTION: MELANOMA RISK DETECTION
FILE REFERENCE: 8795-27U1
CURRENT APPLICATION NUMBER: US/10/108,732
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/279,515
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patent in version 3.1
SEQ ID NO 47
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: hmsHR C-inner sequencing primer 2
US-10-108-732-47

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1133 TCACCTCCAGCTCCA 1147
Db 16 TCACCTCCAGCTCCA 2

RESULT 911
US-10-209-324-32/c
Sequence 32, Application US/10209324
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLAND, Amanda E.
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
FILE REFERENCE: UCSF120-2
CURRENT APPLICATION NUMBER: US/10/209,324
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent in version 3.1
SEQ ID NO 32
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Amplification reaction primer
US-10-209-324-32

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1093 ACCCCACCCCTGGC 1107
Db 15 ACCCTCACCTGGC 1

RESULT 912
US-10-227-563-18207
Sequence 18207, Application US/10227563

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; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
US-10-227-563-18207

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1055 TGGCCCCCAACCCAA 1069
Db 4 TGGCCCCCAACCCAA 18

RESULT 913
US-10-282-174-162/c
; Sequence 162, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; FILE REFERENCE: Associated with Alzheimer's Disease and Other
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-162

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 AGAAAGCCTGGAGT 826
```

```
Db 16 AGAAGCCTGGAGT 2

RESULT 914
US-10-294-040-54/c
; Sequence 54, Application US/10294040
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,040
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1102
; SOFTWARE: Proprietary
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Helicobacter pylori 26695 complete genome.
; FEATURE:
; LOCATION: (101442)...(101459)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
US-10-294-040-54

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
Db 15 ATTTCTTTGGTCTT 1

RESULT 915
US-10-294-040-279/c
; Sequence 279, Application US/10294040
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Helicobacter pylori 26695 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,040
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1102
; SOFTWARE: Proprietary
; SEQ ID NO 279
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Helicobacter pylori 26695 complete genome.
; FEATURE:
; LOCATION: (370226)...(370242)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber =
US-10-294-040-279

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTTGGTCTT 921
Db 15 ATTTCTTTGGTCTT 1

RESULT 916
US-10-310-188-82210/c
; Sequence 82210, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82210
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-82210

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 967 CGGTGGAGTCCCAAG 981
Db 18 CGGTGGAGACCAAG 4

RESULT 917
US-10-349-143-5085
; Sequence 5085, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5085
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18__bind
; OTHER INFORMATION: upstream amplification primer 99-20747 for SEQ 1151,
US-10-349-143-5085

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 TCCAAAGCTCTACTCC 990
Db 4 TCCAAAGCTCTACTCC 18

RESULT 918
US-10-367-892-18207
; Sequence 18207, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18207
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2199746)...(2199763)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 21297
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```
US-10-367-892-18207

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1055 TGGCCCCCAACCCAA 1069
Db 4 TGGCCCCCAACCCAA 18

RESULT 919
US-10-453-792-270/C
; Sequence 270, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-10-453-792-270

Query Match          0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAACAGCA 742
Db 18 GCCAGGAGAACAGCA 4

RESULT 920
US-10-453-792-272/C
```

; Sequence 272, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 35,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4100
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-453-792-272

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
||| |||||
Db 18 GCCATGAGAAACAGA 4

RESULT 921
US-10-453-792-273/c
; Sequence 273, Application US/10453792
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.

; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-453-792-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
||| |||||
Db 18 GCCAGGAGAAACAGA 4

RESULT 922
US-10-464-158-18
; Sequence 18, Application US/10464158
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1
; FILE REFERENCE: ISPH-0749
; CURRENT APPLICATION NUMBER: US/10/464,158
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 09/857,278
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US99/13624
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 09/205,204
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-464-158-18

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 761 ATGAGGTTTCTTTC 775
Db 4 ATGAGGCTTCTTTC 18

RESULT 923
US-10-600-009-162/c
; Sequence 162, Application US/10600009
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Eliiot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Berttram, Iars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-600-009-162

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 812 AGAAGAGCCTGGAGT 826
Db 16 AGAGAGCCTGGAGT 2

RESULT 924
US-10-606-879-270/c
; Sequence 270, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA

QY 728 GCCAGAGAAACAGA 742
Db 18 GCCAAGAGAACAGA 4

RESULT 925
US-10-606-879-272/c
; Sequence 272, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/10/606,879
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/BP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 270:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-10-606-879-270

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGAGAAACAGA 742
Db 18 GCCAAGAGAACAGA 4

RESULT 925
US-10-606-879-272/c
; Sequence 272, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/10/606,879
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
```

;
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 272:
US-10-606-879-272

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCATGAGAAACAGA 4

RESULT 926
US-10-606-879-273/c
; Sequence 273, Application US/10606879
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/606,879
; FILING DATE: 27-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 273:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-10-606-879-273

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 728 GCCAGGAGAAACAGA 742
Db 18 GCCAGGAGAAACAGA 4

RESULT 927
US-60-216-745-8219/c
; Sequence 8219, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaur-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY.
; FILE REFERENCE: 84.US1.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 8219
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-53687 for SEQ 3688,
US-60-216-745-8219

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 931 TCCCTCCTCTTCATT 945
Db 15 TCCCTCCTCTTCATT 1

RESULT 928
US-60-492-056-743/c
; Sequence 743, Application US/60492056
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Timothy Vickers
; APPLICANT: C. Frank Bennett
; APPLICANT: Richard H. Griffey
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS AND COMPOSITIONS FOR USE IN MODULATION OF
; FILE REFERENCE: CORE0016US.L
; CURRENT APPLICATION NUMBER: US/60/492,056
; CURRENT FILING DATE: 2003-08-13
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 18
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-60-492-056-743

Query Match 0.6%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 887 CAGTGTCTGTGCCCC 901
Db 15 CAGTGATGTGCCCC 1

RESULT 929
PCT-US00-22029-11/c
; Sequence 11, Application PC/TUS0022029
; GENERAL INFORMATION:
; APPLICANT: KARLSEN, FRANK
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF THE INDICATORS OF
; TITLE OF INVENTION: CONTAMINATION IN SAMPLES
; FILE REFERENCE: 618123-6
; CURRENT APPLICATION NUMBER: PCT/US00/22029
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/149,365
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli
PCT-US00-22029-11

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1227 CCTGTGGACAGCCCT 1241
Db 19 CCTGTGGACAGCCCT 5

RESULT 930
PCT-US03-03473-41
; Sequence 41, Application PC/TUS0303473
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Platelet Derived Growth
; TITLE OF INVENTION: Factor (PDGF) and Platelet Derived Growth Factor Receptor (PDGFR
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-073 (400/092)
; CURRENT APPLICATION NUMBER: PCT/US03/03473
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 41
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-03473-41

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCGTGGCTTC 1110
Db 1 CCCACCGUGGGCUUC 15

RESULT 931
PCT-US03-03473-352/c
; Sequence 352, Application PC/TUS0303473
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowrira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Platelet Derived Growth
; TITLE OF INVENTION: Factor (PDGF) and Platelet Derived Growth Factor Receptor (PDGFR
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 03-073 (400/092)
; CURRENT APPLICATION NUMBER: PCT/US03/03473
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-03473-352

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CCCACCGTGGCTTC 1110
Db 19 CCCACCGTGGCTTC 5

RESULT 932
PCT-US03-03662-178/c
; Sequence 178, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Express:

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; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-03662-178

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred.No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 774 TCTAAGAGAAAAACA 788
Db 19 TCTAAGAGAAAAACTA 5

RESULT 933
PCT-US03-03662-417
; Sequence 417, Application PC/TUS0303662
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 02-1005-A (400/083)
; CURRENT APPLICATION NUMBER: PCT/US03/03662
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 417
; LENGTH: 19
; TYPE: RNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-03662-417

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred.No. 6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 810 TAAGAAAGCCTCGA 824
Db 2 UAAGAAAAACCCUGGA 16

RESULT 935
PCT-US03-04908-645/C
; Sequence 645, Application PC/TUS0304908
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of BCL2 Gene Expression
; FILE REFERENCE: 02-714-A (400/086)
; CURRENT APPLICATION NUMBER: PCT/US03/04908
; CURRENT FILING DATE: 2003-02-18
```

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; PRIOR APPLICATION NUMBER: US 60/396,905
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 882
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 645
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-04908-645

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```

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 810 TAAGAAAGCCTGGA 824
    ||||| |||||
Db 18 TAAGAAAGCCTGGA 4

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RESULT 936
PCT-US03-40977-26190/c
; Sequence 26190, Application PC/TUS0340977
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: PCT/US03/40977
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26190
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-40977-26190

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```

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGCTGTGCC 899
    ||||| |||||
Db 15 CACAGTGCTGTGCC 1

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RESULT 937
PCT-US03-40978-73310/c
; Sequence 73310, Application PC/TUS0340978
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: PCT/US03/40978
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73310
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-40978-73310

```

```

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 885 CACAGTGCTGTGCC 899
    ||||| |||||
Db 15 CACAGTGCTGTGCC 1

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RESULT 938
US-08-965-620-775/c
; Sequence 775, Application US/08965620
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Wang, David
; APPLICANT: Hudson, Thomas
; TITLE OF INVENTION: Biallelic Markers
; NUMBER OF SEQUENCES: 3817
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,620
; FILING DATE: 06-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,455
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI96-10pA (DUP)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 775:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-965-620-775

```

```

Query Match          0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1012 CCTGAAAAGAGGGG 1026
    ||||| |||||
Db 16 CCTGAAAAGAGGGG 2

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RESULT 939
US-09-634-960A-11/c
; Sequence 11, Application US/09634960A
; GENERAL INFORMATION:

```

```
; APPLICANT: Karlisen, Frank
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF THE INDICATORS OF CONTAMINATION IN I
; FILE REFERENCE: 5775.018
; CURRENT APPLICATION NUMBER: US/09/634,960A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/149,365
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-634-960A-11

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1227 CCTGCGACGACCCCT 1241
Db 19 CCCGCGACGACCCCT 5

RESULT 940
US-10-148-687-55
; SEQUENCE 55: Application US/10148687
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU P04400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-148-687-55

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1068 AAGCTTCAGTCCAC 1082
Db 5 AAGCTTCAGTCCAC 19

RESULT 941
US-10-244-647-598
; SEQUENCE 598: Application US/10244647
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
```

```
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-598

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 26.7%; Pred. No. 6e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTCTTGGTCTTG 923
Db 1 UUUUUUUUGUCUUUG 15

RESULT 942
US-10-244-647-637
; SEQUENCE 637: Application US/10244647
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBHB02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 637
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-637

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 26.7%; Pred. No. 6e+02;
Matches 4; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTGGTCTT 921
Db 5 AUUUUUUUUGUCUU 19

RESULT 943
US-10-244-647-1244/c
; SEQUENCE 1244: Application US/10244647
; GENERAL INFORMATION:
```

APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MH02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1244
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1244

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 909 TTCTCTTGTCCTTG 923
|||||
Db 19 TTCTCTTGTCCTTG 5

RESULT 944
US-10-244-647-1283/c
Sequence 1283, Application US/10244647
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceutical, Inc.
APPLICANT: Morrissey, David
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
FILE REFERENCE: 400/060 (MH02-1000)
CURRENT APPLICATION NUMBER: US/10/244,647
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/393,924
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: PCT US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 1524
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1283
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-1283

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 ATTTCTTGTCCTTG 921
|||||

Db 15 ATTTCTTGTCCTTG 1
RESULT 945
US-10-293-338-2823/c
Sequence 2823, Application US/10293338
GENERAL INFORMATION:
APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2823
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-293-338-2823

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 CTCGACCCCATCCC 1259
|||||
Db 16 CTCGTCCTCCCATCCC 2

RESULT 946
US-10-293-338-3206
Sequence 3206, Application US/10293338
GENERAL INFORMATION:
APPLICANT: RosettaGenomics LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
FILE REFERENCE: 45282
CURRENT APPLICATION NUMBER: US/10/293,338
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 8785
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3206
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-293-338-3206

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1073 TCAGTCCCACTCCAG 1087
|||||
Db 2 TCAGTCCCACTCCAG 16

RESULT 947
US-10-303-778-6522
Sequence 6522, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6522
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens

US-10-303-778-6522

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

QY 878 CAGGCACACAGTGC 892
D5 5 CAGGCATCAGTGC 19

RESULT 948

```

US-10-303-778-11820/c
; Sequence 11820, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11820
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-11820

```

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%;
Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

QY 1253 CCATCCCCAACCCCC 1267
||| ||||||||
Db 16 CCACCCCCAACCCCC 2

RESULT 949

```

US-10-310-188-9763/c
; Sequence 9763, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9763
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9763

```

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

QY 1253 CCATCCCCAACCCCC 1267
Db 19 CCATCCCCAACCCCC 5

RESULT 950

```

RES001, 930
US-10-310-188-21659/c
; Sequence 21659, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETERMINABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487

```

```

; CURRENT APPLICATION NUMBER: US/10/310,188
;
; CURRENT FILING DATE: 2002-12-19
;
; NUMBER OF SEQ ID NOS: 86841
;
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 21659
;
; LENGTH: 19
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-10-310-188-21659

```

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

QY , 1253 CCATCCCCAACCCCC 1267
Db 16 CCACCCCCAACCCCC 2

RESULT 951

```

US-10-310-188-59914
; Sequence 59914, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59914
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-59914

```

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. NO. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

QY 1092 CACCCCAACCTGGG 1106
Db 4 CACCCCAACCTGGG 18

RESULT 952

```

US-10-310-188-72707
; Sequence 72707, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72707
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72707

```

Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels

Qy 1192 GAGGTGGCACCACC 1206
db 2 GATGTGGCACCACC 16

```
RESULT 953
US-10-349-143-7262/c
; Sequence 7262, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7262
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19_bind
; OTHER INFORMATION: upstream amplification primer 99-3335 for SEQ 3328,
US-10-349-143-7262
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 862 AAGGCACCTGAGGAC 876
Db 16 AAGGCACCTGAGAAC 2

RESULT 954
US-10-605-840-3515/c
; Sequence 3515, Application US/10605840
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VACCINIA REGULATORY
; FILE REFERENCE: 55027
; CURRENT APPLICATION NUMBER: US/10/605,840
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 3750
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3515
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-605-840-3515
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 876 CTCAGGCACACAGT 890
Db 18 CTCAGGCTCCAGT 4

RESULT 955
US-10-707-147-1738
; Sequence 1738, Application US/10707147
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; FILE REFERENCE: 49992
; CURRENT APPLICATION NUMBER: US/10/707,147
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 20189
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1738
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-707-147-1738
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1050 GCCCTGCCCCAAA 1064
Db 1 GCCCTGCCCCAAA 15

RESULT 956
US-10-741-600-73310/c
; Sequence 73310, Application US/10741600
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73310
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73310
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGCTGTGCC 899
Db 15 CACAGTGCTTTGCC 1

RESULT 957
US-10-741-601-26190/c
; Sequence 26190, Application US/10741601
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26190
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-26190
Query Match 0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 885 CACAGTGCTGTGCC 899
Db 15 CACAGTGCTTTGCC 1
```

```
RESULT 958
US-10-742-649-20/c
; Sequence 20, Application US/10742649
; GENERAL INFORMATION:
; APPLICANT: Beinfuhr, Claudia
; TITLE OF INVENTION: METHOD FOR SPECIFIC FAST DETECTION OF
; TITLE OF INVENTION: RELEVANT BACTERIA IN DRINKING WATER
; FILE REFERENCE: MAIWAM4.006CL
; CURRENT APPLICATION NUMBER: US/10/742,649
; CURRENT FILING DATE: 2003-12-18
; PRIOR APPLICATION NUMBER: PCT/EP02/06809
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: DE 101 29 411.5
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: DE 101 60 666.4
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-742-649-20

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1010 CACCTGAAAAAGAGG 1024
        |||||
Db       15 CACCGAAAAAGAGG 1

RESULT 959
US-60-082-614-1535/c
; Sequence 1535, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequil
; NUMBER OF SEQUENCES: 2730
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,614
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.020PR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs

Query Match      0.6%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1010 CACCTGAAAAAGAGG 1024
        |||||
Db       15 CACCGAAAAAGAGG 1

RESULT 959
US-60-082-614-1535/c
; Sequence 1535, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequil
; NUMBER OF SEQUENCES: 2730
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,614
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.020PR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1535:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       18 GGTGGAGCTGCAGAA 4

RESULT 961
US-10-317-277A-142
; Sequence 142, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-317-277A-142

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       3 GGTGGAGCTGCAGAA 17

RESULT 961
US-10-317-277A-142
; Sequence 142, Application US/10317277A
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; TITLE OF INVENTION: Modulation of Estrogen-Responsive Finger Protein Expression
; FILE REFERENCE: RTS-0473
; CURRENT APPLICATION NUMBER: US/10/317,277A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-317-277A-142

Query Match      0.6%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 6.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1416 GCTGGAGCTGCAGAA 1430
        |||||
Db       3 GGTGGAGCTGCAGAA 17
```

RESULT 962

PCT-US02-08937-165
; Sequence 165, Application PC/TUS0208937
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: LEINAMYCIN BIOSYNTHESIS GENE CLUSTER AND ITS COMPONENTS AND THEIR
; FILE REFERENCE: 309T-000110PC
; CURRENT APPLICATION NUMBER: PCT/US02/08937
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide PCR primer.
PCT-US02-08937-165

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 872 AGGACTCAGGCACACAG 889
| | | | | | | | | | | | | | | | | |
Db 1 ATGACCCAGGCACCATG 18

RESULT 963

PCT-US02-25943-29066/c
; Sequence 29066, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2810497)...(2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 31120
PCT-US02-25943-29066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCCAGTTCACCTTCAC 1136
| | | | | | | | | | | | | | | | | |
Db 18 GCCCAGTTCGCTTCAC 1

RESULT 964

PCT-US02-25943-51780
; Sequence 51780, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 51780
; LENGTH: 18

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5016571)...(5016588)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 554
PCT-US02-25943-51780

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
| | | | | | | | | | | | | | | | | |
Db 1 CCCAGCTCCACCATCACC 18

RESULT 965

PCT-US02-25943-60330/c
; Sequence 60330, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60330
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5873912)...(5873928)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 646
PCT-US02-25943-60330

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTCACCTCCAGCTCCA 1147
| | | | | | | | | | | | | | | | | |
Db 18 CCATCACCAGCAGCGCA 1

RESULT 966

PCT-US02-34679-341
; Sequence 341, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09

PCT-US02-34679-343
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-341

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CGTGCCAGTCCACCTT 1133
||| ||||| |||||
Db 1 CGAGCCAGATCAACCTT 18

RESULT 967
PCT-US02-34679-343
; Sequence 343, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1116 CGTGCCAGTCCACCTT 1133
||| ||||| |||||
Db 1 CGAGCCAGATCAACCTT 18

RESULT 968
PCT-US98-17838-74
; Sequence 74, Application PC/TUS9817838
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: PCT/US98/17838
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US98-17838-74

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCAACCCCTTC 1270
||| ||||| |||||
Db 1 CCATCCCCAGCCCCATC 18

RESULT 969
PCT-US99-08268-26/c
; Sequence 26, Application PC/TUS9908268
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Sasmor, Susan M.
; APPLICANT: Freier, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
; TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
; FILE REFERENCE: ISIS-3456
; CURRENT APPLICATION NUMBER: PCT/US99/08268
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 09/067,638
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: US 60/081,483
; EARLIER FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 372
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US99-08268-26

```
Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
Db 18 TAGACACCTGGAACAGAG 1

RESULT 970
PCT-US99-08268-221/c
; Sequence 221, Application PC/TUS9908268
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
; TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
; TITLE OF INVENTION: Modulation
; FILE REFERENCE: ISIS-3456
; CURRENT APPLICATION NUMBER: PCT/US99/08268
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 09/067,638
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: US 60/081,483
; EARLIER FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 372
; SEQ ID NO 221
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US99-08268-221

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCAGTTCACCTTCACC 1137
Db 18 CTCATTCCACCTTCACC 1

RESULT 971
PCT-US99-08765A-26/c
; Sequence 26, Application PC/TUS9908765A
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF
; TITLE OF INVENTION: CD40 EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
```

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; APPLICATION NUMBER: PCT/US99/08765A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/071,433
; FILING DATE: March 12, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US99-08765A-26

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
Db 18 TAGACACCTGGAACAGAG 1

RESULT 972
PCT-US99-10260-74
; Sequence 74, Application PC/TUS9910260
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KvLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: PCT/US99/10260
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10260-74

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCAACCCCTTC 1270
Db 1 CCATCCCCAGCCCCATC 18

RESULT 973
US-08-489-967-1
; Sequence 1, Application US/08489967
```

```
/
/
/ GENERAL INFORMATION:
/ APPLICANT: Studier, F. W.
/ APPLICANT: Dunn, John J.
/ TITLE OF INVENTION: SYNTHESIS OF DNA BY HEXAMER LIGATION
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Brookhaven National Laboratory
/ STREET: Building 902C
/ CITY: Upton
/ STATE: New York
/ COUNTRY: US
/ ZIP: 11973
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/489,967
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bogosian, Margaret
/ REGISTRATION NUMBER: 25,324
/ REFERENCE/DOCKET NUMBER: AUI 95-10
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 282-7338
/ TELEFAX: (516) 282-3729
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/
/ US-08-489-967-1
/
/ Query Match 0.6%; Score 13.2; DB 1; Length 18;
/ Best Local Similarity 83.3%; Pred. No. 6.1e+02;
/ Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 965 AACGTGGAGTCAAGC 982
/ Db 1 AACATGGAAGTCGAGC 18
/
/ RESULT 974
/ US-08-969-330-47/c
/ Sequence 47, Application US/08969330
/ GENERAL INFORMATION:
/ APPLICANT: SmithKline Beecham Corporation
/ APPLICANT: Thomas Jefferson University
/ TITLE OF INVENTION: HRAD54
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: U.S.A.
/ ZIP: 19406-0939
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/969,330
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/030,676
/ FILING DATE: November 13, 1996
/
```

```
/
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Han, William T
/ REGISTRATION NUMBER: 34,344
/ REFERENCE/DOCKET NUMBER: ATGS0032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/
/ US-08-969-330-47
/
/ Query Match 0.6%; Score 13.2; DB 1; Length 18;
/ Best Local Similarity 83.3%; Pred. No. 6.1e+02;
/ Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 853 GAGATGTTAAGGGCACT 870
/ Db 18 GATAATGGTTAGGGCACT 1
/
/ RESULT 975
/ US-09-067-638B-26/c
/ Sequence 26, Application US/09067638B
/ GENERAL INFORMATION:
/ APPLICANT: Lex M. Cowser
/ APPLICANT: Brenda F. Baker
/ APPLICANT: John McNeil
/ APPLICANT: Susan M. Preier
/ APPLICANT: Henri M. Sasnor
/ APPLICANT: Douglas G. Brooks
/ APPLICANT: Cara Ohashi
/ APPLICANT: Jacqueline R. Wyatt
/ APPLICANT: Alexander Borchers
/ APPLICANT: Timothy A. Vickers
/ TITLE OF INVENTION: Identification of Genetic
/ TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
/ TITLE OF INVENTION: Generation of Oligonucleotides for Gene
/ TITLE OF INVENTION: Modulation
/ NUMBER OF SEQUENCES: 112
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WOODCOCK WASHBURN KURTZ
/ ADDRESSEE: MACKIEWICZ & NORRIS LLP
/ STREET: 1 LIBERTY PLACE 46TH FLOOR
/ CITY: PHILADELPHIA
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-Windows NT
/ SOFTWARE: WORD PERFECT 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/067,638B
/ FILING DATE: 28-APR-1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/081,483
/ FILING DATE: 13-APR-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: John W. Caldwell
/ REGISTRATION NUMBER: 28,937
/ REFERENCE/DOCKET NUMBER: ISIS-2960
/
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-067-638B-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
| | | | | | | | | | | | | | | | | |
Db 18 TAGACACCTGGACAG 1

RESULT 976
US-09-135-021-72
Sequence 72, Application US/09135021
GENERAL INFORMATION:
APPLICANT: Splawski, Igor
TITLE OF INVENTION: A HOMOLOGOUS MUTATION IN KVLQ1 WHICH CAUSES JERVELL
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021
EARLIER FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-09-135-021-72

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | |
Db 1 CCATCCCCCAGCCCCATC 18

RESULT 977
US-09-295-463-26/c
Sequence 26, Application US/09295463
GENERAL INFORMATION:
APPLICANT: Cowser, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
APPLICANT: Freier, Susan M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3455
CURRENT APPLICATION NUMBER: US/09/295,463
CURRENT FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: US/09/067,638

EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 60/081,483
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 26
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-295-463-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 TCGACACCTGAAAAAGAG 1023
| | | | | | | | | | | | | | | | | |
Db 18 TAGACACCTGGACAG 1

RESULT 978
US-09-295-463-221/c
Sequence 221, Application US/09295463
GENERAL INFORMATION:
APPLICANT: Cowser, Lex M.
APPLICANT: Baker, Brenda F.
APPLICANT: McNeil, John
APPLICANT: Freier, Susan M.
APPLICANT: Sasmor, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Identification of Genetic Targets for Modulation by
TITLE OF INVENTION: Oligonucleotides and Generation of Oligonucleotides for Gene
FILE REFERENCE: ISIS-3455
CURRENT APPLICATION NUMBER: US/09/295,463
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: US/09/067,638
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: US 60/081,483
EARLIER FILING DATE: 1998-04-13
NUMBER OF SEQ ID NOS: 372
SEQ ID NO 221
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-295-463-221

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
| | | | | | | | | | | | | | | | | |
Db 18 CTCTATTCACCTTCACC 1

RESULT 979
US-09-541-946-1083
Sequence 1083, Application US/09541946
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Altschuler, David M.
APPLICANT: Ireland, James S.
APPLICANT: Sklar, Pamela
APPLICANT: Patil, Nila

```
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1083
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1083
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTCTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18
```

```
RESULT 980
US-09-541-946-1090
; Sequence 1090, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1090
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTCTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18

RESULT 981
US-09-541-946-1101
; Sequence 1101, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
```

```
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946
; CURRENT FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2889
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1101
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-541-946-1101
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1197 GGCACCACTCTATCAGG 1214
||| ||||| |||||
Db 1 GGCATCACCTCTCTGGG 18
```

```
RESULT 982
US-09-582-533A-251
; Sequence 251, Application US/09582533A
; GENERAL INFORMATION:
; APPLICANT: VIDER
; TITLE OF INVENTION: METHOD OR IDENTIFYING AND CHARACTERIZING CELLS AND TISSUES
; FILE REFERENCE: 24296
; CURRENT APPLICATION NUMBER: US/09/582,533A
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 251
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-582-533A-251
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1093 ACCCCACCTGGGCTTC 1110
||| ||||| |||||
Db 1 AGCCCAAGCTGGGTTTC 18
```

```
RESULT 983
US-09-868-301-24/c
; Sequence 24, Application US/09868301
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
; FILE REFERENCE: RTSP-0127
; CURRENT APPLICATION NUMBER: US/09/868,301
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Synthetic
US-09-868-301-24

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 CCCAGTTCACCTTCACC 1137
| | | | | | | | | | | | | | | | | |
Db 18 CTCATTCCACCTTCACC 1

RESULT 984

US-09-868-301A-24/c
; Sequence 24, Application US/09868301A

; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
; FILE REFERENCE: RTSP-0127
; CURRENT APPLICATION NUMBER: US/09/868,301A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-868-301A-24

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 CCCAGTTCACCTTCACC 1137
| | | | | | | | | | | | | | | | | |
Db 18 CTCATTCCACCTTCACC 1

RESULT 985

US-10-116-325-26/c
; Sequence 26, Application US/10116325

; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Identification of Genetic Targets For Modulation By Oligonucleotides
; FILE REFERENCE: ISIS026
; CURRENT APPLICATION NUMBER: US/10/116,325
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-10-116-325-26

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1006 TCGACACCTGAAAGAG 1023
| | | | | | | | | | | | | | | | | |
Db 18 TAGACACCTGGACAGAG 1

RESULT 986

US-10-138-316-74
; Sequence 74, Application US/10138316

; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN MINK WHICH CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING KCNE1 AS AN IOT GENE
; FILE REFERENCE: 2323-162
; CURRENT APPLICATION NUMBER: US/10/138,316
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/444,295
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-138-316-74

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1253 CCATCCCCAACCCCTTC 1270
| | | | | | | | | | | | | | | | | |
Db 1 CCATCCCCAGCCCCATC 18

RESULT 987

US-10-227-565-29066/c

; Sequence 29066, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

; FEATURE:
; LOCATION: (2810497)...(2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 311
US-10-227-565-29066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCAGTTCACCTTCAC 1136
 Db 18 GCCAGTTCGTCCTTCAC 1

RESULT 988

US-10-227-565-51780
 ; Sequence 51780, Application US/10227565
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/227,565
 ; CURRENT FILING DATE: 2002-08-26
 ; NUMBER OF SEQ ID NOS: 64158
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 51780
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
 ; FEATURE:
 ; LOCATION: (5016571)...(5016588)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445
 US-10-227-565-51780

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
 Db 1 CCCAGTTCGACATCACC 18

RESULT 989

US-10-227-565-60330/c
 ; Sequence 60330, Application US/10227565
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/227,565
 ; CURRENT FILING DATE: 2002-08-26
 ; NUMBER OF SEQ ID NOS: 64158
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 60330
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
 ; FEATURE:
 ; LOCATION: (5873912)...(5873928)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 64604
 US-10-227-565-60330

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTTCACCTCGAGTCACA 1147
 Db 18 CCATCAGCGCAGCGCA 1

RESULT 990

US-10-266-090-38112/c
 ; Sequence 38112, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN

; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
 ; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
 ; FILE REFERENCE: NADII.058C1
 ; CURRENT APPLICATION NUMBER: US/10/266,090
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US 10/260,703
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/326,117
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 51812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38112
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
 US-10-266-090-38112

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1249 GACCCATCCCAACCCC 1266
 Db 18 GACCACTCTCCACCCC 1

RESULT 991

US-10-266-090-40503
 ; Sequence 40503, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN
 ; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
 ; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
 ; FILE REFERENCE: NADII.058C1
 ; CURRENT APPLICATION NUMBER: US/10/266,090
 ; CURRENT FILING DATE: 2002-10-03
 ; PRIOR APPLICATION NUMBER: US 10/260,703
 ; PRIOR FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/326,117
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 51812
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 40503
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
 US-10-266-090-40503

Query Match 0.6%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1122 CAGTTCACCTTCACCTC 1139
 Db 1 CAGTCCACCAACCACTC 18

RESULT 992

US-10-266-090-47008
 ; Sequence 47008, Application US/10266090
 ; GENERAL INFORMATION:
 ; APPLICANT: GOFF, STEPHEN
 ; APPLICANT: BONAN, CAROLINE
 ; APPLICANT: COLBERT, MICHELLE
 ; APPLICANT: WANG, RONG-LIN
 ; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE

```
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47008
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-47008
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1129 ACCTTCACCTCCAGCTCC 1146
|||||
DB 1 ACCTCCACCTCTCTCTCC 18
```

```
RESULT 993
US-10-266-090-51552
; Sequence 51552, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51552
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-51552
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1128 CACCTTCACCTCCAGCTC 1145
|||||
DB 1 CACCAGCTCTCTCTCTCC 18
```

```
RESULT 994
US-10-266-090-51728
; Sequence 51728, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
```

```
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51728
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-51728
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1129 ACCTTCACCTCCAGCTCC 1146
|||||
DB 1 ACCTCCACCTCTCTCTCC 18
```

```
RESULT 995
US-10-282-174-341
; Sequence 341, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-341
```

```
Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1116 CGTCCACGATTCACCTT 1133
```

Db 1 CGAGCCGAGATCAACCTT 18
|| ||||| || |||||

RESULT 996

US-10-282-174-343
; Sequence 343, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Vellicelebi, Gonul
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-343

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1116 CGTCCGAGTTCACCTT 1133
|| ||||| || |||||

Db 1 CGAGCCGAGATCAACCTT 18

RESULT 997

US-10-293-338-2066
; Sequence 2066, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-2066

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1251 CCCCATCCCCAACCCCTT 1268
|| ||||| || |||||

Db 1 CCCCTCCCCCACCCCTT 18

RESULT 998

US-10-293-338-6601
; Sequence 6601, Application US/10293338
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 45282
; CURRENT APPLICATION NUMBER: US/10/293,338
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 8785
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6601
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-338-6601

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 889 GTGCTGTTCACCTTGGC 906
|| ||||| || |||||

Db 1 GTGCTGTTCACCTTGGC 18

RESULT 999

US-10-303-778-3233
; Sequence 3233, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3233
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-3233

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 909 TTTCTTTGGTTCCTTGCCT 926
|| ||||| || |||||

Db 1 TTTCTTTGGCATTTCTT 18

RESULT 1000

US-10-303-778-4618/c
; Sequence 4618, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4618
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4618

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1248 CGACCCCATCCCAACCC 1265
Db 18 CCACCCCAACCCCAACCC 1

RESULT 1001
US-10-303-778-4666/c
; Sequence 4666, Application US/10303778

; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4666
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4666

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1248 CGACCCCATCCCAACCC 1265
Db 18 CCACCCCAACCCCAACCC 1

RESULT 1002
US-10-303-778-4999/c
; Sequence 4999, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4999
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-4999

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1128 CACCTTCACCTCCAGCTC 1145
Db 18 CACCCCAACCCCAACCTC 1

RESULT 1003
US-10-303-778-8192/c

; Sequence 8192, Application US/10303778
; GENERAL INFORMATION:

; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8192
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-8192

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1119 GCCCAGTTCACCTTCAC 1136
Db 18 GCCCAGTTCACCTTCAC 1

RESULT 1004
US-10-310-188-4288/c
; Sequence 4288, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4288
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-4288

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 908 TTTTCITTTGCTTTGCC 925
Db 18 TTTTCITTTGCTTTGCC 1

RESULT 1005
US-10-310-188-5478
; Sequence 5478, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5478
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5478

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 909 TTCTTTTGGCTTTCCT 926
Db 1 TTCTTTTGGCTTTCCT 18

RESULT 1006
US-10-310-188-6210
; Sequence 6210, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6210
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-6210

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1243 GCTCGACCCCATCCCT 1260
Db 1 GCTCGACCCCATCCCT 18

RESULT 1007
US-10-310-188-9659/c
; Sequence 9659, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9659
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9659

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1248 CGACCCCATCCCAACCC 1265
Db 1 CGACCCCATCCCAACCC 18

RESULT 1008
US-10-310-188-9706/c
; Sequence 9706, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9706

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-9706

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1248 CGACCCCATCCCAACCC 1265
Db 1 CGACCCCATCCCAACCC 18

RESULT 1009
US-10-310-188-10527/c
; Sequence 10527, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10527
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-10527

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1128 CACCTTCACCTCCAGCTC 1145
Db 18 CACCTTCACCTCCAGCTC 1

RESULT 1010
US-10-310-188-11033
; Sequence 11033, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11033
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-11033

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1235 CAGCCCTCGCTCCGACC 1252
Db 1 CAGCCCTCGCTCCGACC 18

RESULT 1011
US-10-310-188-17069
; Sequence 17069, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics

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; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17069
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-17069

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1223 CCATCTTGGCAGAGCCC 1240
      ||||| ||||| |||||
Db 1 CCGTCGGTGGCAGAGCCC 18

RESULT 1012
US-10-310-188-26440
; Sequence 26440, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26440
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-26440

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1230 TGGCAGAGCCCTGGCCCTC 1247
      ||||| ||||| |||||
Db 1 TGGCAGAGCTGGCCAC 18

RESULT 1013
US-10-310-188-42111/c
; Sequence 42111, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42111
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-42111

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1247 CCGACCCCATCCCAACC 1264
      ||||| ||||| |||||
Db 1 CCGACCCCATCCCGCCC 1
```

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Db 18 CCGGCCCATCCCGCCC 1

RESULT 1014
US-10-310-188-42218/c
; Sequence 42218, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42218
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-42218

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1139 CCAGCTCCACCTATACCC 1156
      ||||| ||||| |||||
Db 18 CCAGCCCGAGCTTACCC 1

RESULT 1015
US-10-310-188-51868/c
; Sequence 51868, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51868
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-51868

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1244 CCTCCGACCCCATCCCA 1261
      ||||| ||||| |||||
Db 18 CCTCCGACCCCATCCCA 1

RESULT 1016
US-10-310-188-58107/c
; Sequence 58107, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58107
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-58107
```

US-10-310-188-58107

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 913 TTGTGCTTTGCTTTTA 930
||| ||||| |||
Db 18 TTCTCTTTGCTTTCTTA 1

RESULT 1017

US-10-310-188-64553
; Sequence 64553, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64553
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64553

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1242 CGCTCCGACCCATCCC 1259
||| ||||| |||
Db 1 CCGCTCTACCCCTCCC 18

RESULT 1018

US-10-310-188-64750
; Sequence 64750, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64750
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64750

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1581 CGGCCCCGCGCCCTCCC 1598
||| ||||| |||
Db 1 CGCCCCGCGCCCTCCC 18

RESULT 1019

US-10-310-188-69028/c
; Sequence 69028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69028
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-69028

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1254 CATCCCAACCCCTTCA 1271
||| ||||| |||
Db 18 CATCCCTGCCCATTTCA 1

RESULT 1020

US-10-310-188-71360/c
; Sequence 71360, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71360
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-71360

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 909 TTCTTTGGTCTTTGCTT 926
||| ||||| |||
Db 18 TTCTTTCTTTTGTGCTT 1

RESULT 1021

US-10-310-188-72865/c
; Sequence 72865, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72865
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-72865

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1252 CCCATCCCAACCCCTT 1269
||| ||||| |||
Db 18 CCCACCCCAACCCCTT 1

```
RESULT 1022
US-10-310-188-75117/c
; Sequence 75117, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75117
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-75117

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1242 CGCCTCCGACCCCATCCC 1259
Db 18 CGCCCCCACCCTCCCTCC 1

RESULT 1023
US-10-310-188-77971/c
; Sequence 77971, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77971
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-77971

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 743 ACACCGTGGCACCCTGCC 760
Db 18 ACCCGTGGCACCCTGCC 1

RESULT 1024
US-10-310-188-80411
; Sequence 80411, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80411
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-80411

Query Match      0.6%; Score 13.2; DB 1; Length 18;
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```
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 870 TGAGGACTCAGGCACCAC 887
Db 1 TGGGACTCAGGCACCAC 18

RESULT 1025
US-10-310-188-85848
; Sequence 85848, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85848
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85848

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 869 CTGAGGACTCAGGCACCAC 886
Db 1 CAGAGGACGAGGCACCAC 18

RESULT 1026
US-10-310-188-85920/c
; Sequence 85920, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85920
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-85920

Query Match      0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 927 TTATCCCTCCTCTTCAT 944
Db 18 TTCATCCCTCCTCTTCCT 1

RESULT 1027
US-10-310-188-86807/c
; Sequence 86807, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86807
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-86807

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1211 AGGGGCTGACCCCATCC 1228
||||| ||||| |||||
Db 18 AGGGGCTGAGCCATCC 1

RESULT 1028

US-10-314-657-165
; Sequence 165, Application US/10314657
; GENERAL INFORMATION:

; APPLICANT: SHEN, Ben
; APPLICANT: CHENG, Yi-Qiang
; APPLICANT: TANG, Gong-Li
; TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide
; TITLE OF INVENTION: Synthases and Methods of Use
; FILE REFERENCE: 054030-0021
; CURRENT APPLICATION NUMBER: US/10/314,657
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: PCT/US02/08937
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/278,935
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Streptomyces atroolivaceus
US-10-314-657-165

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 872 AGGACTCAGGCACACAG 889
||||| ||||| |||||
Db 1 ATGACCCAGGCACACTG 18

RESULT 1029

US-10-349-143-4110/c
; Sequence 4110, Application US/10349143
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4110
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens

; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13332 for SEQ 176,
US-10-349-143-4110

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 813 GAAAAGCCTGAGTGCAC 830
||||| ||||| |||||
Db 18 GAAAAGCCTCACTGCAC 1

RESULT 1030

US-10-349-143-4877/c
; Sequence 4877, Application US/10349143
; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4877
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens

; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-18386 for SEQ 943,
US-10-349-143-4877

Query Match 0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTTCACCTCCAGTCCA 1147
||||| ||||| |||||
Db 18 CTTTACCTCCACCTCCA 1

RESULT 1031

US-10-367-832A-29066/c
; Sequence 29066, Application US/10367832A
; GENERAL INFORMATION:

; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 29066
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2810497) ... (2810514)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-367-832A-29066

```

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1119 GCCCAGTTCACCTTCAC 1136
DB 18 GCCCAGTTCGCTTCAC 1

RESULT 1032
US-10-367-832A-51780
; Sequence 51780, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 51780
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5016571)...(5016588)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 55445
US-10-367-832A-51780

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1120 CCCAGTTCACCTTCACC 1137
DB 1 CCCAGTTCGACCATCACC 18

RESULT 1033
US-10-367-832A-60330/c
; Sequence 60330, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 60330
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (5873912)...(5873928)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 64604
US-10-367-832A-60330

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1130 CCTTCACCTCCAGCTCCA 1147
DB 18 CCATCACCAGCGGCA 1

RESULT 1034
US-10-368-643-74
; Sequence 74, Application US/10368643
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.

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; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-163
; CURRENT APPLICATION NUMBER: US/10/368,643
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/597,731
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: US 09/135,010
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: US 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: US 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: US 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: US 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-368-643-74

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 CCATCCCCACCCCGCTTC 1270
DB 1 CCATCCCCAGCCCCATC 18

RESULT 1035
US-10-388-263-26/c
; Sequence 263, Application US/10388263
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freiler, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-26

Query Match
Best Local Similarity 0.6%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```



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; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-600-009-343

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1116 CGTCCCGAGTTCACCTT 1133
Db 1 CGAGCCGAGTCAACCTT 18

RESULT 1040
US-60-216-745-8632
; Sequence 8632, Application US/60216745
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Abderrahim, Hadi
; APPLICANT: Dufaire-Gare, Isabelle
; TITLE OF INVENTION: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
; FILE REFERENCE: 84.Usi.PRO
; CURRENT APPLICATION NUMBER: US/60/216,745
; CURRENT FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 13665
; SOFTWARE: Patent.pm
; SEQ ID NO 8632
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-31024 for SEQ 4101,
US-60-216-745-8632

Query Match          0.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1020 AGAGGGGAGCTTGAGG 1037
Db 1 AGAGGAGGAGTTGATGG 18

RESULT 1041
US-09-949-427-355/c
; Sequence 355, Application US/09949427
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Luisi, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafari, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NPUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-355

Query Match          0.6%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 36 GGAGCCTCAGTCCAGAGA 53
Db 20 GGAGCCTGAGTCTCTCAGA 3

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RESULT 1042
US-09-949-427A-355/c
; Sequence 355, Application US/09949427A
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Luisi, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafari, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 8038 02810-0014
; CURRENT APPLICATION NUMBER: US/09/949,427A
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 355
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427A-355

Query Match          0.6%; Score 13.2; DB 1; Length 21;

```

```
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 GGAGCCTCAGTCACGAGA 53
DB 20 GGAGCCTCAGTCCTCAGA 3

RESULT 1043
US-09-949-428-355/c
; Sequence 355, Application US/09949428
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusia, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
; FILE REFERENCE: 02810.0014.NPUS01
; CURRENT APPLICATION NUMBER: US/09/949,428
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-355

Query Match 0.6%; Score 13.2; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 GGAGCCTCAGTCACGAGA 53
DB 20 GGAGCCTCAGTCCTCAGA 3

RESULT 1044
US-10-355-577-560795
; Sequence 560795, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-560795

Query Match 0.6%; Score 13.2; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2075 ACTGTCCTAAGCAGGGG 2092
DB 4 ACTGTCGCAAGGAGGGG 21

RESULT 1045
```

```
US-60-353-987-560795
; Sequence 560795, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 560795
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-560795

Query Match 0.6%; Score 13.2; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2075 ACTGTCCTAAGCAGGGG 2092
DB 4 ACTGTCGCAAGGAGGGG 21

RESULT 1046
US-08-529-190A-4/c
; Sequence 4, Application US/08529190A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,190A
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: THERE-005AX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-529-190A-4
```

Query Match 0.6%; Score 13; DB 1; Length 24;
 Best Local Similarity 76.2%; Pred. No. 8e+02;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCCTGGAGCTGTGTGG 316
 ||| ||||| |||||
 Db 23 TGGTGCTGGAGGTGCGGTGG 3

RESULT 1047

US-08-733-369A-60/c
 ; Sequence 60, Application US/08733369A
 ; GENERAL INFORMATION:
 ; APPLICANT: Masucci, Maria G.
 ; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERRING
 ; TITLE OF INVENTION: INVISIBILITY TO THE IMMUNE SYSTEM.
 ; NUMBER OF SEQUENCES: 123
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordperfect 6.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/733,369A
 ; FILING DATE: 17 October, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/522,995
 ; FILING DATE: 01-SEP-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/529,190
 ; FILING DATE: 15-SEP-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: SE 95013249
 ; FILING DATE: 10-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB96/00876
 ; FILING DATE: 10-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams, Kathleen M.
 ; REGISTRATION NUMBER: 34,380
 ; REFERENCE/DOCKET NUMBER: 95-1391-D
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-9100
 ; TELEFAX: 617-345-9111
 ; INFORMATION FOR SEQ ID NO: 60:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; US-08-733-369A-60

Query Match 0.6%; Score 13; DB 1; Length 24;
 Best Local Similarity 76.2%; Pred. No. 8e+02;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCCTGGAGCTGTGTGG 316
 ||| ||||| |||||
 Db 23 TGGTGCTGGAGGTGCGGTGG 3

RESULT 1048

US-08-970-900-55/c
 ; Sequence 55, Application US/08970900
 ; GENERAL INFORMATION:

; APPLICANT: Masucci, Maria G.
 ; TITLE OF INVENTION: FUSION PROTEINS HAVING INCREASED HALF-LIVES.
 ; NUMBER OF SEQUENCES: 91
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02111

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordperfect 6.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/970,900
 ; FILING DATE: 14-NOV-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/030,986
 ; FILING DATE: 15-NOV-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/048,945
 ; FILING DATE: 25-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams, Kathleen M.
 ; REGISTRATION NUMBER: 34,380
 ; REFERENCE/DOCKET NUMBER: 3255/59831
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-9100
 ; TELEFAX: 617-345-9111
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 24 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; US-08-970-900-55

Query Match 0.6%; Score 13; DB 1; Length 24;
 Best Local Similarity 76.2%; Pred. No. 8e+02;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 296 TGCTCCTGGAGCTGTGTGG 316
 ||| ||||| |||||
 Db 23 TGGTGCTGGAGGTGCGGTGG 3

RESULT 1049

PCT-US02-25940-3485/c
 ; Sequence 3485, Application PC/TUS0225940
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
 ; FILE REFERENCE: Jim Zeigler Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: PCT/US02/25940
 ; CURRENT FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 25502
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 3485
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
 ; FEATURE:
 ; LOCATION: (437846)...(437861)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 40;
 ; PCT-US02-25940-3485

Query Match 0.6%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 6.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

RESULT 1054
US-08-733-369A-63/c
; Sequence 63, Application US/08733369A
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES CONFERRING
; INVULNERABILITY TO THE IMMUNE SYSTEM.
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,369A
; FILING DATE: 17 October, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/522,995
; FILING DATE: 01-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/529,190
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 95013249
; FILING DATE: 10-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00876
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 95-1391-D
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-733-369A-63

Query Match 0.6%; Score 12.8; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 295 GTGCTCTGGAGCTGTGGTGGGA 318
Db 24 GTGGAGCTGGAGTGGCGGTGGAA 1

RESULT 1055
US-08-970-900-57/c
; Sequence 57, Application US/08970900
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: FUSION PROTEINS HAVING INCREASED HALF-LIVES.
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathleen M. Williams, Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: Massachusetts

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; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,900
; FILING DATE: 14-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,986
; FILING DATE: 15-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,945
; FILING DATE: 25-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3255/59831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-970-900-57

Query Match 0.6%; Score 12.8; DB 1; Length 24;
Best Local Similarity 70.8%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 295 GTGCTCTGGAGCTGTGGTGGGA 318
Db 24 GTGGAGCTGGAGTGGCGGTGGAA 1

RESULT 1056
PCT-US02-34679-162
; Sequence 162, Application PC/TUS0234679
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308PC
; CURRENT APPLICATION NUMBER: PCT/US02/34679
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28

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; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-34679-162

Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ACTCCAGGCTTCAC 1094
||| |||||
Db 2 ACTCCAGGCTTCTC 15

RESULT 1057
US-10-282-174-162
; Sequence 162, Application US/10282174
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-162

Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ACTCCAGGCTTCAC 1094
||| |||||
Db 2 ACTCCAGGCTTCTC 15

RESULT 1058
US-10-600-009-162
; Sequence 162, Application US/10600009

; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308B
; CURRENT APPLICATION NUMBER: US/10/600,009
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/282,174
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-600-009-162

Query Match 0.6%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 7.8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1081 ACTCCAGGCTTCAC 1094
||| |||||
Db 2 ACTCCAGGCTTCTC 15

RESULT 1059
PCT-US02-29102-30/c
; Sequence 30, Application PC/TUS0229102
; GENERAL INFORMATION:
; APPLICANT: Applied Biosystems
; APPLICANT: Bolchakova, Elena V.
; APPLICANT: Rozzelle, James E.
; TITLE OF INVENTION: A Novel DNA Polymerase from the Thermophilic Thermus Scotoeductu
; FILE REFERENCE: 1560.002W01
; CURRENT APPLICATION NUMBER: PCT/US02/29102
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/334489
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/322218
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus scotoeductus
PCT-US02-29102-30

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1060

PCT-US02-37657-51/c
; Sequence 51, Application PC/TUS0237657
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768WO
; CURRENT APPLICATION NUMBER: PCT/US02/37657
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus brockianus
PCT-US02-37657-51

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1061

PCT-US02-37764-30/c
; Sequence 30, Application PC/TUS0237764
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 4777WO
; CURRENT APPLICATION NUMBER: PCT/US02/37764
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
PCT-US02-37764-30

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1062

US-10-302-817A-51/c
; Sequence 51, Application US/10302817A
; GENERAL INFORMATION:

; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US
; CURRENT APPLICATION NUMBER: US/10/302,817A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 60/334,434
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus brockianus
US-10-302-817A-51

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

RESULT 1063

US-10-303-109A-30/c
; Sequence 30, Application US/10303109A
; GENERAL INFORMATION:
; APPLICANT: BOLCHAKOVA, Elena
; APPLICANT: ROZZELLE, James
; TITLE OF INVENTION: Thermus Oshimai Nucleic Acid Polymerases
; FILE REFERENCE: 4777US
; CURRENT APPLICATION NUMBER: US/10/303,109A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/334,798
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Thermus oshimai
US-10-303-109A-30

Query Match 0.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 301 CTGGAGCTGTTGGTGGG 317
Db 17 CTGGAGGTGGAGGTGGG 1

Search completed: March 1, 2004, 15:37:18
Job time : 29 secs

Tue Mar 2 06:29:53 2004

schultz451-1.rge

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PAVCO, DENNIS MACEJAK
PI C12N9/00.A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT virus)'
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Location/Qualifiers
1..14
/organism="unidentified"
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Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 3 GCGGCTCCCGC 14
RESULT 1274
BD209419 14 bp RNA linear PAT 17-JUL-2003
LOCUS Enzymatic nucleic acid treatment of diseases or conditions related
DEFINITION to hepatitis C virus infection.
ACCESSION BD209419.1 GI:33019189
VERSION BD209419.1
KEYWORDS JP 2002512791-A/3009.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt, L., McSwiggen, J.A., Roberts, B., Pavco, P.A. and Macejak, D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 3009 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/3009
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545391
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO, DENNIS MACEJAK
PI C12N9/00.A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT virus)'
FEATURES
Location/Qualifiers
1..14
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1216 GGTGACCCCATC 1227
DB 3 GGTGACCCCATC 14
RESULT 1275
S81271 14 bp mRNA linear PRI 07-MAY-1993
LOCUS mitochondrial acetoacetyl-coenzyme A thiolase [human, mRNA Partial
DEFINITION Mutant, 14 nt].
ACCESSION S81271
VERSION S81271.1 GI:245356
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 14)
AUTHORS Fukao, I., Yamaguchi, S., Orii, T., Schutzgens, R.B., Osumi, T. and Hashimoto, T.
TITLE Identification of three mutant alleles of the gene for mitochondrial acetoacetyl-coenzyme A thiolase. A complete analysis of two generations of a family with 3-ketothiolase deficiency
JOURNAL J. Clin. Invest. 89 (2), 474-479 (1992)
MEDLINE 92147861
PUBMED 1346617
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 81271] from the original journal article. This sequence comes from Figure 2.
COMMENT exon 8 skipping
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Query Match 0.5%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 6.5e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 919 CTTTGCCTTTA 930
DB 13 CTTGCGCTTTA 2
Search completed: March 1, 2004, 15:13:28
Job time : 29 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 15:39:29 ; Search time 0.001 Seconds
(without alignments)
1456.514 Million cell updates/sec

Title: us-09-695-451-1
Perfect score: 8161
Sequence: 1 Gggcccgatctgaacc.....tacactaaattctgaagt 2161

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 337 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 44 summaries

Database : rnnp.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	18	0.8	18	1	US-10-774-118-15
C 2	14.8	0.7	21	1	Sequence 15, Appl
C 3	14.8	0.7	21	1	Sequence 23831, A
C 4	12.2	0.6	17	1	Sequence 23832, A
C 5	12.2	0.5	17	1	PCT-US03-31862-1271
C 6	11.8	0.5	15	1	Sequence 1271, Ap
C 7	11.4	0.5	15	1	Sequence 1272, Ap
C 8	11.2	0.5	16	1	Sequence 16, Appl
C 9	9.8	0.5	14	1	Sequence 20, Appl
C 10	9.2	0.4	14	1	Sequence 49917, A
C 11	9.2	0.4	15	1	Sequence 2689, Ap
C 12	9	0.4	17	1	Sequence 2689, Ap
C 13	9	0.4	17	1	Sequence 20, Appl
C 14	8.8	0.4	12	1	Sequence 1271, Ap
C 15	8.8	0.4	12	1	Sequence 1272, Ap
C 16	8.8	0.4	12	1	Sequence 19, Appl
C 17	8.8	0.4	12	1	Sequence 23, Appl
C 18	8.8	0.4	12	1	Sequence 25, Appl
C 19	8.8	0.4	12	1	Sequence 80, Appl
C 20	8.8	0.4	12	1	Sequence 4, Appl
C 21	8.6	0.4	16	1	Sequence 15, Appl
C 22	8.6	0.4	21	1	Sequence 15, Appl
C 23	8.6	0.4	21	1	Sequence 15, Appl
C 24	8.4	0.4	10	1	Sequence 23831, A
C 25	8.4	0.4	10	1	Sequence 6, Appl
C 26	8.4	0.4	10	1	Sequence 7, Appl
C 27	8.4	0.4	10	1	Sequence 7, Appl
C 28	8.4	0.4	11	1	Sequence 38, Appl
C 29	8.4	0.4	11	1	Sequence 38, Appl
C 30	8.4	0.4	12	1	Sequence 25, Appl
C 31	8.4	0.4	12	1	Sequence 25, Appl
C 32	8.4	0.4	12	1	Sequence 10, Appl
C 33	8.4	0.4	12	1	PCT-US03-26191A-10
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Sequence 11, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-774-118-15/c
; GENERAL INFORMATION:
; APPLICANT: Le Junming
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human Tumor Necrosis Factor
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-038
; CURRENT APPLICATION NUMBER: US/10/774,118
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US 09/756,301
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-10-774-118-15

Query Match 0.8%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGCTACCCAGATT 852
DB 18 TTGTGCTACCCAGATT 1

RESULT 2

US-10-770-726-23831/c

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,066
; FILING DATE: 05-Jan-2001
; APPLICATION NUMBER: 06/848,013
; FILING DATE: 2001-05-07
; APPLICATION NUMBER: 07/830,886
; FILING DATE: 04-FEB-1992
; APPLICATION NUMBER: 07/748,277
; FILING DATE: 21-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kegan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 02939.04541
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-768-089-16

Query Match 0.5%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 GCTGTTGCCCTGGT 905
Db 15 GCTGTTGGCTCTGGT 1

RESULT 7
US-09-892-360-20/c
; Sequence 20, Application US/09892360
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, GEORGES
; APPLICANT: ROMBY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; TITLE OF INVENTION: RILUZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-892-360-20

Query Match 0.5%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 3.6;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 869 CTGAGGACTCAGG 881
Db 15 CTGAGGACTCAGG 3

RESULT 8
US-10-767-471-49917/c
; Sequence 49917, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49917
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-49917

Query Match 0.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 5.5;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1266 CTTCCAGAAGTGGGAG 1281
Db 16 CTTCCAGAAGCGGGAG 1

RESULT 9
PCT-US03-31862-2689
; Sequence 2689, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: NaPro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2689
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-31862-2689

Query Match 0.5%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 12;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 GGCACCACAGTGC 892
Db 1 GACACCACGGTGC 13

RESULT 10
PCT-US03-31862-2689/c
; Sequence 2689, Application PC/TUS0331862
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF DELAWARE
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; FILE REFERENCE: NaPro-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31862
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 2707
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2689
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; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-31862-2689

Query Match 0.4%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1822 TGCACCGTGGGCTC 1835
Db 14 TGCACCGTGGGTC 1

RESULT 11

US-09-892-360-20
; Sequence 20, Application US/09892360

; GENERAL INFORMATION:

; APPLICANT: LAZDUNSKI, MICHEL

; APPLICANT: LESAGE, FLORIAN

; APPLICANT: ROMEY, GEORGES

; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND APARCHIDONIC ACID-SENSITIVE

; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND

; TITLE OF INVENTION: RILUZOLE

; FILE REFERENCE: 1256-R-00

; CURRENT APPLICATION NUMBER: US/09/892,360

; PRIOR FILING DATE: 2001-06-27

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-892-360-20

Query Match 0.4%; Score 9.2; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1606 CCCAGTCTTCTCAG 1619
Db 2 CCCTGACTCTCAG 15

RESULT 12

PCT-US03-31862-1271

; Sequence 1271, Application PC/TUS0331862

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF DELAWARE

; APPLICANT: KMEC, ERIC B.

; APPLICANT: VAN BRABANT, ANJA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN

; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

; FILE REFERENCE: Napro-18 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/31862

; CURRENT FILING DATE: 2003-10-07

; PRIOR APPLICATION NUMBER: US 60/453,360

; PRIOR FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: US 60/416,983

; PRIOR FILING DATE: 2002-10-07

; NUMBER OF SEQ ID NOS: 2707

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1271

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Triticum aestivum

PCT-US03-31862-1271

Query Match 0.4%; Score 9; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 864 GGGCACTGAGGACTCAG 880
Db 1 GGGCACTGAGTGTGTCAG 17

RESULT 13

PCT-US03-31862-1272/C

; Sequence 1272, Application PC/TUS0331862

; GENERAL INFORMATION:

; APPLICANT: UNIVERSITY OF DELAWARE

; APPLICANT: KMEC, ERIC B.

; APPLICANT: VAN BRABANT, ANJA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN

; TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION

; FILE REFERENCE: Napro-18 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/31862

; CURRENT FILING DATE: 2003-10-07

; PRIOR APPLICATION NUMBER: US 60/453,360

; PRIOR FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: US 60/416,983

; PRIOR FILING DATE: 2002-10-07

; NUMBER OF SEQ ID NOS: 2707

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1272

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Triticum aestivum

PCT-US03-31862-1272

Query Match 0.4%; Score 9; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 864 GGGCACTGAGGACTCAG 880
Db 17 GGGCACTGAGTGTGTCAG 1

RESULT 14

US-10-484-991-19

; Sequence 19, Application US/10484991

; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND

; APPLICANT: HUMAN SERVICES

; APPLICANT: Klinman, Dennis M.

; APPLICANT: Gursel, Ihsan

; APPLICANT: Puri, Raj K.

; APPLICANT: Kawakami, Koji

; APPLICANT: Ishii, Ken J.

; APPLICANT: Joshi, Bharat H.

; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY

; TITLE OF INVENTION: DELIVER CPG OLIGONUCLEOTIDES IN VIVO

; FILE REFERENCE: 4239-67620

; CURRENT APPLICATION NUMBER: US/10/484,991

; CURRENT FILING DATE: 2004-01-26

; PRIOR APPLICATION NUMBER: US 60/308,283

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: PCT/US02/24235

; PRIOR FILING DATE: 2002-07-29

; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 19

; LENGTH: 12

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Cpg oligodeoxynucleotide

US-10-484-991-19

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1083 TCCAGGCTTCAC 1094
||| |||||
Db 1 TCGAGGCTTCTC 12

RESULT 15

US-10-484-991-19/c
; Sequence 19, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-19

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 813 GAAAGCGCTGGA 824
||| |||||
Db 12 GAGAGCCTCGA 1

RESULT 16

US-10-484-991-23/c
; Sequence 23, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23

; LENGTH: 12

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1282 GACAGCGCCAC 1293
||| |||||
Db 1 12 GTCAGCGCCGAC 1

RESULT 17

US-10-484-991-25
; Sequence 25, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-25

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1282 GACAGCGCCAC 1293
||| |||||
Db 1 12 GTCAGCGCCGAC 12

RESULT 18

US-10-484-991-80/c
; Sequence 80, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620

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; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-80

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1027 GAGCTTGAAGGA 1038
Db 12 GAGCTGAAGCA 1

RESULT 19
US-10-451-323-4/c
; Sequence 4, Application US/10451323
; GENERAL INFORMATION:
; APPLICANT: MARCHAL, GILLES
; APPLICANT: ROMAIN, FELIX
; APPLICANT: PESCHER, PASCALE
; TITLE OF INVENTION: IMMUNOGENIC GLYCOPETIDES, SCREENING, PREPARATION AND USES
; FILE REFERENCE: 238218US0PCT
; CURRENT APPLICATION NUMBER: US/10/451,323
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: PCT/FR01/04100
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: FR 00/16808
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-10-451-323-4

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1166 GTCCCAACTTTG 1177
Db 12 GGCCCAACGTTG 1

RESULT 20
US-10-767-471-49917
; Sequence 49917, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49917
; LENGTH: 16
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-49917

Query Match      0.4%; Score 8.8; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 524 CCGCTTCAGAAA 535
Db 4 CCGCTTCTGGAA 15

RESULT 21
US-10-774-118-15
; Sequence 15, Application US/10774118
; GENERAL INFORMATION:
; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-038
; CURRENT APPLICATION NUMBER: US/10/774,118
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 09/756,301
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR oligonucleotides
US-10-774-118-15

Query Match      0.4%; Score 8.6; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1441 CTGCGCGAGGCGCAA 1455
Db 4 CTGGGGTAGGCACAA 18

RESULT 22
US-10-770-726-23831
; Sequence 23831, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

```
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23831
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-23831

Query Match      0.4%; Score 8.6; DB 1; Length 21;
Best Local Similarity 73.3%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1519 GGACGGCTGCTCCGC 1533
Db 7 GCACGAGTCTCAGC 21

RESULT 23
US-10-770-726-23832
; Sequence 23832, Application US/10770726
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23832
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-770-726-23832

Query Match      0.4%; Score 8.6; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1519 GGACGGCTGCTCCGC 1533
Db 5 GCACGAGUCCUACG 19

RESULT 24
US-10-652-361-6
; Sequence 6, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUNDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGGG 84
Db 1 AGAGGAGGAG 10

RESULT 25
US-10-652-361-7/c
; Sequence 7, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOUNDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-7

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGGG 84
Db 10 AGAGGAGGAG 1

RESULT 26
US-10-652-430-6
; Sequence 6, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUNDENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-6
```

Query Match 0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGG 84
Db 1 AGAGGAGG 10

RESULT 27
US-10-652-430-7/c
; Sequence 7, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOODENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-7

Query Match 0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 75 AGAGGAGGG 84
Db 10 AGAGGAGG 1

RESULT 28
US-10-660-897-38
; Sequence 38, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-38

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 29
US-10-660-897-38/c
; Sequence 38, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-38

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCTCTCTC 942
Db 11 CCTCTCTCTC 2

RESULT 30
US-10-484-991-23
; Sequence 23, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF SPERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67630
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 23
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-23

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1796 GTCAGCGCTG 1805
||| |||||
Db 1 GTCGGCGCTG 10

RESULT 31
US-10-484-991-25/c
; Sequence 25, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-25

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1796 GTCAGCGCTG 1805
||| |||||
Db 12 GTCGGCGCTG 3

RESULT 32
PCT-US03-26191A-10/c
; Sequence 10, Application PC/TUS0326191A
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC
; APPLICANT: ARAI, AKIKO
; TITLE OF INVENTION: STARS - A MUSCLE-SPECIFIC ACTIN-BINDING PROTEIN
; FILE REFERENCE: MYOG:037WO
; CURRENT APPLICATION NUMBER: PCT/US03/26191A
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/404,706
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
PCT-US03-26191A-10

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1182 TCACGCGCAGA 1191
||| |||||
Db 12 TCACGCGCAGA 3

RESULT 33
US-10-484-991-50/c
; Sequence 50, Application US/10484991
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Gursel, Ihsan
; APPLICANT: Puri, Raj K.
; APPLICANT: Kawakami, Koji
; APPLICANT: Ishii, Ken J.
; APPLICANT: Joshi, Bharat H.
; TITLE OF INVENTION: USE OF STERICALLY STABILIZED CATIONIC LIPOSOMES TO EFFICIENTLY
; FILE REFERENCE: 4239-67620
; CURRENT APPLICATION NUMBER: US/10/484,991
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 60/308,283
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/US02/24235
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CpG oligodeoxynucleotide
US-10-484-991-50

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1258 CCCAACCCCC 1267
||| |||||
Db 12 CCCAACGCC 3

RESULT 34
US-10-660-897-11
; Sequence 11, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: QUADRUPEX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
/
/ FEATURE:
/ OTHER INFORMATION: quadruplex forming sequence
US-10-660-897-11

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 35
US-10-660-897-11/c
; Sequence 11, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: quadruplex forming sequence
US-10-660-897-11

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 933 CCTCTCTCTC 942
Db 11 CCTCTCTCTC 2

RESULT 36
US-10-660-897-19/c
; Sequence 19, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-19

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1058 CCCCAAAACC 1067
Db 12 CCCCAAAACC 3

RESULT 37
US-10-660-897-24
; Sequence 24, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-24

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1859 GAGGATGAGG 1868
Db 2 GAGGAGGAGG 11

RESULT 38
US-10-660-897-24/c
; Sequence 24, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; TITLE OF INVENTION: QUADRUPLIX FORMING NUCLEIC ACIDS AND MODULATORS THEREOF
; FILE REFERENCE: 532232000800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60/410,475
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-660-897-24

Query Match      0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 12;
```

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 942

Db 11 CCTCCTCTTC 2

RESULT 39

US-10-660-897-32
; Sequence 32, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-32

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1859 GAGGATGAGG 1868

Db 2 GAGGAGGAGG 11

RESULT 40

US-10-660-897-32/c
; Sequence 32, Application US/10660897
; GENERAL INFORMATION:
; APPLICANT: Jin, Cheng
; APPLICANT: Chung, Mary
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Whitten, Jeffrey
; APPLICANT: Farrell, Thomas
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR IDENTIFYING
; FILE REFERENCE: 53223200800
; CURRENT APPLICATION NUMBER: US/10/660,897
; CURRENT FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: motif
US-10-660-897-32

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 942

Db 11 CCTCCTCTTC 2

RESULT 41

US-10-652-361-6/c
; Sequence 6, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOODENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-6

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 940

Db 8 CCTCCTCTTC 1

RESULT 42

US-10-652-361-7
; Sequence 7, Application US/10652361
; GENERAL INFORMATION:
; APPLICANT: WOODENBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND KITS FOR ASSEMBLING PROBES
; FILE REFERENCE: 5049 US
; CURRENT APPLICATION NUMBER: US/10/652,361
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-361-7

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 933 CCTCCTCTTC 940

Db 3 CCTCCTCTTC 10

RESULT 43

US-10-652-430-6/c
; Sequence 6, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-6

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 CCTCCTCT 940
|||||||
Db 8 CCTCCTCT 1

RESULT 44
US-10-652-430-7
; Sequence 7, Application US/10652430
; GENERAL INFORMATION:
; APPLICANT: WOUDEBERG, TIMOTHY M.
; APPLICANT: BAHATT, DAR
; APPLICANT: SHARAF, MUHAMMAD A.
; APPLICANT: LIU, TIMOTHY Z.
; APPLICANT: ERMAKOV, SERGUEI
; APPLICANT: CONNELL, CHARLES R.
; APPLICANT: HYLDIG-NIELSEN, JENS J.
; TITLE OF INVENTION: MULTIPLEX DETECTION COMPOSITIONS, METHODS, AND KITS
; FILE REFERENCE: 5023 US
; CURRENT APPLICATION NUMBER: US/10/652,430
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-652-430-7

Query Match 0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 933 CCTCCTCT 940
|||||||
Db 3 CCTCCTCT 10

Search completed: March 1, 2004, 15:39:30
Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 15:41:44 ; Search time 1 Seconds
(without alignments)

3.916 Million cell updates/sec

Title: us-09-695-451-1

Perfect score: 2161

Sequence: 1 cggccagtgatctgaacc.....tacactaaattctgaagtt 2161

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 91 seqs, 906 residues

Total number of hits satisfying chosen parameters: 182

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 170 summaries

Database : rst.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.4	0.8	19	1	ACCESSION:AZ788326
C 2	11.4	0.5	14	1	ACCESSION:CA798290
C 3	11.4	0.5	16	1	ACCESSION:AL696566
C 4	11	0.5	12	1	ACCESSION:BH169696
C 5	10.2	0.5	16	1	ACCESSION:AL696566
C 6	10	0.5	19	1	ACCESSION:AZ788326
C 7	9.8	0.5	13	1	ACCESSION:BQ589768
C 8	9.8	0.5	13	1	ACCESSION:BH170808
C 9	9.4	0.4	12	1	ACCESSION:BG925521
C 10	9.4	0.4	13	1	ACCESSION:BG926067
C 11	9.4	0.4	13	1	ACCESSION:BQ59423
C 12	9	0.4	9	1	ACCESSION:CF307276
C 13	9	0.4	9	1	ACCESSION:CF307431
C 14	9	0.4	11	1	ACCESSION:CF339065
C 15	9	0.4	11	1	ACCESSION:CF339065
C 16	9	0.4	11	1	ACCESSION:BQ585943
C 17	9	0.4	11	1	ACCESSION:BQ593914
C 18	9	0.4	12	1	ACCESSION:BQ592925
C 19	9	0.4	12	1	ACCESSION:BQ594497
C 20	9	0.4	12	1	ACCESSION:BQ595544
C 21	8.8	0.4	12	1	ACCESSION:BQ587870
C 22	8.8	0.4	12	1	ACCESSION:BQ592925
C 23	8.8	0.4	12	1	ACCESSION:BQ594497
C 24	8.8	0.4	12	1	ACCESSION:BQ595544
C 25	8.8	0.4	12	1	ACCESSION:CF282215
C 26	8.8	0.4	13	1	ACCESSION:BQ589768
C 27	8.8	0.4	13	1	ACCESSION:BG926067
C 28	8.4	0.4	10	1	ACCESSION:CF921234
C 29	8.4	0.4	10	1	ACCESSION:CK298980
C 30	8.4	0.4	11	1	ACCESSION:BM395228
C 31	8.4	0.4	11	1	ACCESSION:BQ590709
C 32	8.4	0.4	11	1	ACCESSION:BM395226
C 33	8.4	0.4	12	1	ACCESSION:BQ587288

ACCESSION:BQ587706	1	12	0.4	8.4	34	C
ACCESSION:BQ589761	1	12	0.4	8.4	35	C
ACCESSION:BQ591624	1	12	0.4	8.4	36	C
ACCESSION:AQ050979	1	12	0.4	8.4	37	C
ACCESSION:B07312	1	12	0.4	8.4	38	C
ACCESSION:CF339091	8	8	0.4	8	39	C
ACCESSION:CF277997	8	8	0.4	8	40	C
ACCESSION:CF301888	8	8	0.4	8	41	C
ACCESSION:CF302851	8	8	0.4	8	42	C
ACCESSION:CF312818	8	8	0.4	8	43	C
ACCESSION:CF309109	9	9	0.4	8	44	C
ACCESSION:CF312817	9	9	0.4	8	45	C
ACCESSION:CF318771	9	9	0.4	8	46	C
ACCESSION:CF330649	9	9	0.4	8	47	C
ACCESSION:CF333615	10	10	0.4	8	48	C
ACCESSION:CA794390	10	10	0.4	8	49	C
ACCESSION:CF322692	11	11	0.4	8	50	C
ACCESSION:BG925521	12	12	0.4	8	51	C
ACCESSION:BQ587288	12	12	0.4	8	52	C
ACCESSION:BQ587706	12	12	0.4	8	53	C
ACCESSION:BQ585423	13	13	0.4	8	54	C
ACCESSION:BG927412	11	11	0.4	7.8	55	C
ACCESSION:BG927896	11	11	0.4	7.8	56	C
ACCESSION:BM395997	11	11	0.4	7.8	57	C
ACCESSION:BM395997	11	11	0.4	7.8	58	C
ACCESSION:BQ585943	11	11	0.4	7.8	59	C
ACCESSION:BQ593914	11	11	0.4	7.8	60	C
ACCESSION:BU238234	11	11	0.4	7.8	61	C
ACCESSION:CF323154	11	11	0.4	7.8	62	C
ACCESSION:CF543031	11	11	0.4	7.8	63	C
ACCESSION:BQ587870	12	12	0.4	7.8	64	C
ACCESSION:BQ589761	12	12	0.4	7.8	65	C
ACCESSION:B07312	12	12	0.4	7.8	66	C
ACCESSION:AL394689	9	9	0.3	7.6	67	C
ACCESSION:CF307276	9	9	0.3	7.4	68	C
ACCESSION:CF307431	9	9	0.3	7.4	69	C
ACCESSION:CA850813	9	9	0.3	7.4	70	C
ACCESSION:CF313414	9	9	0.3	7.4	71	C
ACCESSION:CF313414	9	9	0.3	7.4	72	C
ACCESSION:CF323490	9	9	0.3	7.4	73	C
ACCESSION:CF307092	9	9	0.3	7.4	74	C
ACCESSION:CF322585	9	9	0.3	7.4	75	C
ACCESSION:CF322585	9	9	0.3	7.4	76	C
ACCESSION:CF325534	9	9	0.3	7.4	77	C
ACCESSION:CF325534	9	9	0.3	7.4	78	C
ACCESSION:CF325652	9	9	0.3	7.4	79	C
ACCESSION:CF325652	9	9	0.3	7.4	80	C
ACCESSION:BG925375	10	10	0.3	7.4	81	C
ACCESSION:BM396082	10	10	0.3	7.4	82	C
ACCESSION:BM396082	10	10	0.3	7.4	83	C
ACCESSION:BM396082	10	10	0.3	7.4	84	C
ACCESSION:CF311011	10	10	0.3	7.4	85	C
ACCESSION:CF311011	10	10	0.3	7.4	86	C
ACCESSION:CA794390	10	10	0.3	7.4	87	C
ACCESSION:BM395226	11	11	0.3	7.4	88	C
ACCESSION:BM395226	11	11	0.3	7.4	89	C
ACCESSION:BQ591624	12	12	0.3	7.4	90	C
ACCESSION:CF339091	12	12	0.3	7.4	91	C
ACCESSION:CF295648	8	8	0.3	7	92	C
ACCESSION:CF921494	8	8	0.3	7	93	C
ACCESSION:CA851350	8	8	0.3	7	94	C
ACCESSION:CF313731	8	8	0.3	7	95	C
ACCESSION:CA851674	9	9	0.3	7	96	C
ACCESSION:BM396043	10	10	0.3	7	97	C
ACCESSION:BM396043	10	10	0.3	7	98	C
ACCESSION:CF323895	10	10	0.3	7	99	C
ACCESSION:CF323895	10	10	0.3	7	100	C
ACCESSION:CF336905	10	10	0.3	7	101	C
ACCESSION:BM395228	11	11	0.3	7	102	C
ACCESSION:BG927412	11	11	0.3	7	103	C
ACCESSION:BG927896	11	11	0.3	7	104	C
ACCESSION:CF323154	11	11	0.3	7	105	C
ACCESSION:CF282215	12	12	0.3	7	106	C

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c 107 6.8 0.3 10 1 BG925375
c 108 6.8 0.3 10 1 CF333615
c 109 6.8 0.3 10 1 ACCESSION:CF333615
c 110 6.8 0.3 10 1 ACCESSION:CF336905
c 111 6.8 0.3 11 1 ACCESSION:BQ590709
c 112 6.8 0.3 11 1 ACCESSION:CF322692
c 113 6.8 0.3 12 1 ACCESSION:AQ050979
c 114 6.8 0.3 13 1 ACCESSION:BM170808
c 115 6.8 0.3 14 1 ACCESSION:CF798290
c 116 6.4 0.3 8 1 CF305141
c 117 6.4 0.3 8 1 ACCESSION:CF305141
c 118 6.4 0.3 8 1 ACCESSION:CF306116
c 119 6.4 0.3 8 1 ACCESSION:CF306116
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c 122 6.4 0.3 8 1 ACCESSION:CF322514
c 123 6.4 0.3 8 1 ACCESSION:CF322514
c 124 6.4 0.3 8 1 ACCESSION:CF322653
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c 126 6.4 0.3 8 1 ACCESSION:CF323889
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c 128 6.4 0.3 8 1 ACCESSION:CF324406
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c 136 6.4 0.3 8 1 ACCESSION:CF338362
c 137 6.4 0.3 8 1 ACCESSION:CF339016
c 138 6.4 0.3 8 1 ACCESSION:CF339699
c 139 6.4 0.3 8 1 ACCESSION:CF340204
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c 141 6.4 0.3 8 1 ACCESSION:CF340204
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c 155 6.4 0.3 10 1 ACCESSION:CF340204
c 156 6.4 0.3 10 1 ACCESSION:CF340204
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c 158 6.2 0.3 11 1 ACCESSION:CF340204
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ALIGNMENTS

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RESULT 1
AZ788326/c
LOCUS AZ788326 DNA 19 bp
DEFINITION 2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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```
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
```

```
clone UUGC2M0035P16 F, genomic survey sequence.
AZ788326
AZ788326.1 GI:12928014
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: P column: 16
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0035P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
FEATURES
source
```

```
Query Match 0.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. NO. 0.0068;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 987 CTCATTCTTGTGGGA 1004
DB 19 CTCATTCTTGTGGGA 2
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```
RESULT 2
CA798290
LOCUS CA798290 14 bp mRNA linear EST 05-DEC-2002
DEFINITION CA798290 (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_611 5', mRNA sequence.
```

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ACCESSION CA798290
VERSION CA798290.1 GI:26055376
KEYWORDS EST.
SOURCE Theobroma cacao (cacao)
ORGANISM Theobroma cacao
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
          Theobroma.
REFERENCE 1 (bases 1 to 14)
AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
         Retzel, E.R. and Jones, C.A.
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
JOURNAL Planta 216 (2), 255-264 (2002)
MEDLINE 22337596
PUBMED 12447539
COMMENT Contact: Jones, Paul
         3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
         Tel: +44 1664 416644
         Email: Paul.Jones@eu.affm.com
         Seq primer: T3.
FEATURES
    source
        1..14
            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
            /db_xref="taxon:3641"
            /clone="Cac BL 611"
            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"
            /lab_host="Xl-1 Blue MRF"
            /clone_lib="Cac_BL (Bean and Leaf from Amelonado type
            Cacao)"
            /notes="Vector: pBK-CMV; Bean and leaf tissue from an
            Amelonado type Cacao tree."
Query Match 0.5%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 0.99;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1143 CTCGACCTATACC 1155
Db 1 CTCGACCTATACC 13

RESULT 3
ACCESSION AI696566/c
LOCUS AI696566
DEFINITION tx60806.x1 NCI_CGAP Utl1 Homo sapiens cDNA clone IMAGE:2273987 3,
similar to TR:Q15662 Q15662 TRANSFORMATION-RELATED PROTEIN ;, mRNA
sequence.
ACCESSION AI696566
VERSION AI696566.1 GI:4984466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-remail.nih.gov
         Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
         Emerit-Buck, M.D., Ph.D.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: Greg Lennon, Ph.D.
         DNA Sequencing by: Washington University Genome Sequencing Center

```

```

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert length: 1662 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2273987"
                /tissue_type="well-differentiated endometrial
                adenocarcinoma 7 pooled tumors"
                /lab_host="DH10B"
                /clone_lib="NCI_CGAP Utl1"
                /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
                Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
                Average insert size 1.75 kb. Life Technologies catalog #:
                11538-014"
Query Match 0.5%; Score 11.4; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 GGCACCACAGTGCT 893
Db 14 GCCACCACAGTGCT 1

RESULT 4
ACCESSION BH169696
LOCUS BH169696
DEFINITION 12-bp DNA linear GSS 03-OCT-2001
          SALK_001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis
          thaliana genomic clone SALK_001766, genomic survey sequence.
ACCESSION BH169696
VERSION BH169696.1 GI:15905071
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 12)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
         Gadrinab, C., Jeske, A., Karnes, M., Kim, C.-J., Parker, H., Prednis, L.,
         Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
         Contact: Joseph R. Ecker
         Salk Institute Genomic Analysis Laboratory (SIGAL)
         The Salk Institute for Biological Studies
         10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
         Tel: 858 453 4100 x1752
         Fax: 858 558 6379
         Email: ecker@salk.edu
         This is single pass sequence recovered from the left border of
         TDNA.
Class: TDNA tagged.
    Location/Qualifiers
        1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="SALK_001766"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can

```

be found at http://signal.salk.edu/tdna_protocols.html

Query Match 0.5%; Score 11; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1055 TGGCCCCAAC 1065
 |||||
 Db 1 TGGCCCCAAC 11

RESULT 5
 LOCUS AI696566 16 bp mRNA linear EST 16-DEC-1999
 DEFINITION tx60f06.x1 NCI_CGAP Utl Homo sapiens cDNA clone IMAGE:2273987 3' similar to TR:Q15662 Q15662 TRANSFORMATION-RELATED PROTEIN ; , mRNA sequence.

ACCESSION AI696566
 VERSION AI696566
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 16)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmer-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 CDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1662 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2273987"
 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Utl"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

Query Match 0.5%; Score 10.2; DB 1; Length 16;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 192 AGCACTGCGCTGCCA 207
 |||||
 Db 1 AGCACTGNGGTGCCA 16

RESULT 6
 LOCUS AZ788326 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0035P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035P16 F, genomic survey sequence.

ACCESSION AZ788326
 VERSION AZ788326.1 GI:12928014

KEYWORDS EST.

KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: P column: 16
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0035P16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 10; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 47;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 956 ATCGCTACCAACGGTGA 973
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 Db 1 ATTCCCAACCAATGA 18

RESULT 7
 LOCUS BQ589768 13 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012680-024-020-D03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-020-D03 5-PRIME, mRNA sequence.

ACCESSION BQ589768
 VERSION BQ589768.1 GI:26119351
 KEYWORDS EST.

```

SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
REFERENCE   1 (bases 1 to 13)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
              Drugowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Kadelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 13 Std Error: 0.00
              Plate: 20 Row: D Column: 03
              Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES    Location/Qualifiers
             1..13
             /organism="Beta vulgaris"
             /mol_type="mRNA"
             /cultivar="KWS2320 (double haploid, monogerm breeding
             line)"
             /db_xref="GABI:190356"
             /db_xref="taxon:161934"
             /clone="024-020-D03"
             /tissue_type="storage root"
             /lab_host="EMDH10B"
             /clone_lib="MPIZ-ADIS-024-storage root"
             /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
             cDNA library from sugar beet, library provided by KWS
             Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
             b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
             orientation:
             SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
             Sequencing granted in the context of the GABI-Beet
             project, local PI: Dr. Katharina Schneider, coordinator:
             Prof. Christian Jung; Sequence submission managed by
             RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 932 CCTCTCTCTTCAT 944
Db 1 CCTCTCTCTTGAT 13

RESULT 8
BH170808/c
LOCUS      BH170808
DEFINITION SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_003378, genomic survey sequence.
ACCESSION  BH170808.1 GI:15906490
VERSION     BH170808
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1 (bases 1 to 13)
REFERENCE   1 (bases 1 to 13)
AUTHORS     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
              Gardinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
              Shinn,P., Zimmerman,J. and Ecker,J.R.
              A Sequence-Indexed Library of Insertion Mutations in the

```

```

JOURNAL     Arabidopsis Genome
COMMENT      Unpublished (2001)
              Contact: Joseph R. Ecker
              Salk Institute Genomic Analysis Laboratory (SIGAL)
              The Salk Institute for Biological Studies
              10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
              Tel: 858 453 4100 x1752
              Fax: 858 558 6379
              Email: ecker@salk.edu
              This is single pass sequence recovered from the left border of
              TDNA.
              Class: TDNA tagged.
FEATURES    Location/Qualifiers
             1..13
             /organism="Arabidopsis thaliana"
             /mol_type="genomic DNA"
             /strain="Columbia 0"
             /db_xref="taxon:3702"
             /clone="SALK_003378"
             /clone_lib="Arabidopsis thaliana TDNA insertion lines"
             /note="PCR was performed on Arabidopsis thaliana lines
             each of which contains one or more TDNA insertion
             elements. The resultant fragment for each line was
             directly sequenced to determine the genomic sequence at
             the site of insertion. Details of the protocols used can
             be found at http://signal.salk.edu/tdna_protocols.html"
Query Match 0.5%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1131 CTTCACTCCAGC 1143
Db 13 CTTCACTCCAGC 1

RESULT 9
BG925521
LOCUS      BG925521
DEFINITION HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION  BG925521
VERSION     BG925521.1 GI:14320044
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
              Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
              Lark,M.W.
              Identification and initial characterization of 5000 expressed
              sequenced tags (ESTs) each from adult human normal and
              osteoarthritic cartilage cDNA libraries
              Osteoarthr. Cartil. 9 (7), 641-653 (2001)
              21482651
              11597177
              Contact: Sanjay Kumar
              UW2109
              GlaxoSmithKline
              709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
              Tel: 610-270-7245
              Fax: 610-270-5598
              Email: sanjay.kumar-lsgsk.com
              Seq primer: T7.
FEATURES    Location/Qualifiers
             1..12
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /tissue_type="cartilage"
             /lab_host="E.coli DH10 B"

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/clone_lib="HNC (Human Normal Cartilage)"
/notes="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

Query Match      0.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 5.4;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1130 CTTTCACTCC 1140
Db 2 CTTTCCCTCC 12

RESULT 10
BG926067/c
LOCUS
DEFINITION HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG926067
VERSION BG926067.1 GI:14320590
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
FEATURES
source
1..13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/clone_lib="HNC (Human Normal Cartilage)"
/notes="vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

Query Match      0.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1271 AGAAGTGGGAG 1281
Db 11 AGAAGGGGGAG 1

RESULT 11
BQ595423/c
LOCUS
DEFINITION E012693-024-022-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-N20 5-PRIME, mRNA sequence.
ACCESSION BQ595423
VERSION BQ595423.1 GI:26125006
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Euphorbiales; Euphorbiaceae; Euphorbia.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 22 Row: N Column: 20
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
FEATURES
source
1..13
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191428"
/db_xref="taxon:161934"
/clone="024-022-N20"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/notes="vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 10;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 967 CGGTGGAGTCC 977
Db 13 CGGTGGATTC 3

RESULT 12
CF307276
LOCUS
DEFINITION HDAL--06-D23.g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library 1 (HDAL) Oryza sativa cDNA clone HDAL--06-D23, mRNA
sequence.
ACCESSION CF307276
VERSION CF307276.1 GI:33679037
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. . 9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL--06-D23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9
|||||

RESULT 13

CF307431

LOCUS

DEFINITION HDAL--06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--06-K23, mRNA sequence.

ACCESSION

CF307431

VERSION CF307431.1 GI:33679192

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. . 9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL--06-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9
|||||

RESULT 14

CF339065

LOCUS

DEFINITION CF339065 11 bp mRNA linear EST 18-AUG-2003
Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 11)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnamhggbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. . 11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 AGGTGGCAC 1201

Db 1 AGGTGGCAC 9
|||||

RESULT 15

CF339065/c

LOCUS

DEFINITION CF339065 11 bp mRNA linear EST 18-AUG-2003
Oryza sativa cDNA clone RCL1--03-K22, mRNA sequence.

ACCESSION

CF339065

KEYWORDS

EST.

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SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 11)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES   Location/Qualifiers
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                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="RCL1-03-K22"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli: SOLR"
                /clone_lib="Regenerated callus lambda phage cDNA library
                (RCL1)"
                /notes="Vector: pBluescript SK(+); Site.1: SstI; Site.2:
                XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                end with SstI and 3' end with XhoI site. Callus was
                induced on 2N6 media for 30 days and cultured for 36hrs on
                regenerated media"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 AAGTGCAC 444
Db 11 AAGTGCAC 3

RESULT 16
BQ585943
LOCUS      E012531-024-014-K17-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-014-K17 5-PRIME, mRNA sequence.
ACCESSION  BQ585943
VERSION     BQ585943.1 GI:26115525
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 11)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            22362189
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaar@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaar@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

FEATURES   Location/Qualifiers
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                line)"
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                /clone="024-014-K17"
                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-leaf"
                /note="Vector: pCMVSPORT6; Site.1: Sali; Site.2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                Project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GGACGCGTG 1527
Db 2 GGACGCGTG 10

RESULT 17
BQ593914
LOCUS      S015507-024-025-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-025-N20 5-PRIME, mRNA sequence.
ACCESSION  BQ593914
VERSION     BQ593914.1 GI:26123497
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 11)
            Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            22362189
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaar@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaar@mpiz-koeln.mpg.de
            Insert Length: 11 Std Error: 0.00

FEATURES   Location/Qualifiers
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                /mol_type="mRNA"
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                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-leaf"
                /note="Vector: pCMVSPORT6; Site.1: Sali; Site.2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                Project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database:http://gabi.rzpd.de"

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/notes="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GGACGCGTG 1527
Db 1 GGACGCGTG 9

RESULT 18
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DEFINITION E012123-024-028-F05-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-028-F05 5-PRIME, mRNA sequence.
ACCESSION  BQ592925
VERSION     BQ592925.1 GI:26122508
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
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                /lab_host="EMDH10B"
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                /note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
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                Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GGACGCGTG 1527
Db 11 GGACGCGTG 3

RESULT 19
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cDNA clone 024-024-P14 5-PRIME, mRNA sequence.
ACCESSION  BQ594497
VERSION     BQ594497.1 GI:26124080
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@mpiz-koeln.mpg.de
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                1..12
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                /note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GGACGCGTG 1527

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TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PubMed
12472698
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 28 row: F column: 05

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
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/lab_host="EMDH10B"
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/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCTCGCCTCCG 1249
||| ||| |||
Db 1 CCCACGCGTCG 12

RESULT 23
BQ594497
LOCUS
DEFINITION
E012444-024-024-P14-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-P14 5-PRIME, mRNA sequence.
ACCESSION
BQ594497
VERSION
BQ594497.1 GI:26124080
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM

12 bp mRNA linear EST 06-DEC-2002
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Contact: Weissshaar B

TITLE
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fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PubMed
12472698
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 24 row: P column: 14
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
source

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/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1238 CCTCGCCTCCG 1249
||| ||| |||
Db 1 CCCACGCGTCG 12

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BQ595544/c
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cDNA clone 024-022-A12 5-PRIME, mRNA sequence.
ACCESSION
BQ595544
VERSION
BQ595544.1 GI:26125127
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM

12 bp mRNA linear EST 06-DEC-2002
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Contact: Weissshaar B

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PubMed
12472698
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weissshaar@mpiz-koeln.mpg.de
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Plate: 22 row: A column: 12

Seq primer: SP6; CATACGATTAGTGACACTATAG.

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/cultivar="KWS2320 (double haploid, monogerm breeding

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/lab_host="EMDH10B"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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    12 CCCACGCGTCGC 1

Db 12 CCCACGCGTCGC 1

RESULT 25
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DEFINITION
14ETL--09-K01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORyza sativa cDNA clone 14ETL--09-K01, mRNA sequence.
ACCESSION
CF282215
VERSION
CF282215.1 GI:33659602
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..12
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 26
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LOCUS
DEFINITION
BQ589768-024-020-D03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
ACCESSION
BQ589768
VERSION
BQ589768.1 GI:26119351
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 20 row: D column: 03
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES
source
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190356"
/db_xref="taxon:161934"
/clone="024-020-D03"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1014 TGAAAAGAGAGG 1025
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    12 TCAAGAGAGAGG 1

Db 12 TCAAGAGAGAGG 1

RESULT 27
BQ926067
LOCUS
DEFINITION
BQ926067 HNC23-1-B9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BQ926067

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VERSION      BG926067.1  GI:14320590
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 13)
AUTHORS      Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
              Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
              Lark,M.W.
TITLE        Identification and initial characterization of 5000 expressed
              sequenced tags (ESTs) each from adult human normal and
              osteoarthritic cartilage cDNA libraries
JOURNAL      Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE      21482651
PUBMED       11597177
COMMENT      Contact: Sanjay Kumar
              UW2109
              GlaxoSmithKline
              709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
              Tel: 610-270-7245
              Fax: 610-270-5598
              Email: sanjay_kumar-1@gsk.com
              Seq primer: T7.
              Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="cartilage"
                /lab_host="E.coli DH10 B"
                /clone_lib="HNC (Human Normal Cartilage)"
                /notes="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                Directional"

Query Match      0.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1126 TCCACCTTCACC 1137
Db 2 TCCCCCTTCTCC 13

RESULT 28
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LOCUS      gmhrw3-07_B06_1_046 Soybean root hair subtracted cDNA library
DEFINITION gmhrw3 Glycine max cDNA, mRNA sequence.
ACCESSION  CF921234
VERSION     CF921234
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
REFERENCE    1 (bases 1 to 10)
AUTHORS      Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
TITLE        Expressed sequence tags from soybean root hair subtractive cDNA
              library
JOURNAL      Unpublished (2003)
COMMENT      Contact: Gary Stacey
              University of Missouri
              108 Waters Hall, Columbia, MO 65211, USA
              Tel: 573-884-4752
              Fax: 573-882-0588
              Email: stacey@missouri.edu
              Single pass sequence
              Seq primer: T7.
              Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:82"
                /tissue_type="root hairs"
                /clone_lib="Soybean root hair subtracted cDNA library
                gmhrw3"
                /notes="Organ: root hairs; Vector: pCE2-1 Topo; cDNA clones
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                Bradyrhizobium japonicum for 3 hours."

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1179 GGCTCCCGC 1188
Db 10 GGATCCCGC 1

RESULT 29
CK298980
LOCUS      EST761694 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMDU48 3'
              end, mRNA sequence.
ACCESSION  CK298980
VERSION     CK298980.1  GI:39886896
KEYWORDS    EST.
SOURCE      Nicotiana benthamiana
ORGANISM    Nicotiana benthamiana
REFERENCE    1 (bases 1 to 10)
AUTHORS      Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
              Staskawicz,B., Jin,H. and Baker,B.
TITLE        Generation of EST sequences from Nicotiana benthamiana
              Unpublished (2003)
JOURNAL      Other_ESTs: EST761693
COMMENT      Contact: Robin Buell
              The Institute for Genomic Research
              9712 Medical Center Dr, Rockville, MD 20850, USA
              Email: potato-array@tigr.org
              Clones can be requested from TIGR via potato@tigr.org
              Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
              Location/Qualifiers
                1..10
                /organism="Nicotiana benthamiana"
                /mol_type="mRNA"
                /db_xref="taxon:4100"
                /clone_lib="NEMDU48"
                /tissue_type="abiotic and biotic stress-treated leaves,
                callus tissue and root tissue"
                /lab_host="DH10B-Tona"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomat 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."

Query Match      0.4%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES
source

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QY      1964 AGTTTTTTTTT 1973
Db      1 ATTTTITTTT 10

RESULT 30
BM395228/c
LOCUS   50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395228
VERSION 1
KEYWORDS
SOURCE   Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 11)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
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Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1211 AGGGGGCTGA 1220
Db      10 AGGGGGCAGA 1

RESULT 31
BQ590709/c
LOCUS   BQ590709
DEFINITION
E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION
BQ590709
VERSION 1
KEYWORDS
SOURCE   Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
12472698
PUBMED
COMMENT
Contact: Weisshaar B

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:189410"
/db_xref="taxon:161934"
/clone="024-018-024"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
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Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      10 TCCAAGCTCT 1

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LOCUS   BM395226
DEFINITION
50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM395226
VERSION 1
KEYWORDS
SOURCE   Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 11)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES
source
Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1211 AGGGGGCTGA 1220
Db      10 AGGGGGCAGA 1

RESULT 31
BQ590709/c
LOCUS   BQ590709
DEFINITION
E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION
BQ590709
VERSION 1
KEYWORDS
SOURCE   Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 11)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
MEDLINE
12472698
PUBMED
COMMENT
Contact: Weisshaar B

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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 436 AAGTCCAC 445
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Db 11 AAGGCCACA 2

RESULT 33
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LOCUS
DEFINITION BQ587288 12 bp mRNA linear EST 06-DEC-2002
clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
ACCESSION BQ587288
VERSION BQ587288.1 GI:26116870
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS BQ587288
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT 22362189
12472698

FEATURES
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/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: PCWSPOR6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 808 TGTAAGAAA 817
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Db 12 TGGAGAAA 3

RESULT 35
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LOCUS
DEFINITION BQ589761 12 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-020-P03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ589761
VERSION BQ589761.1 GI:26119344
KEYWORDS EST.

RESULT 34
BQ587706/c
LOCUS

DEFINITION BQ587706 12 bp mRNA linear EST 06-DEC-2002
clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ587706
VERSION BQ587706.1 GI:26117288
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS BQ587706
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT 22362189
12472698

FEATURES
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/tissue_type="leaf"
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/note="Vector: PCWSPOR6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 808 TGTAAGAAA 817
||| |||||
Db 12 TGGAGAAA 3

RESULT 35
BQ589761
LOCUS
DEFINITION BQ589761 12 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-020-P03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION BQ589761
VERSION BQ589761.1 GI:26119344
KEYWORDS EST.

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SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 12)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 12 Std Error: 0.00
              Plate: 20 row: P column: 03
              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES     Location/Qualifiers
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              /db_xref="taxon:161934"
              /clone="024-020-P03"
              /tissue_type="storage root"
              /lab_host="EMDH10B"
              /clone_lib="MPIZ-ADIS-024-storage root"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
              Query Match      0.4%; Score 8.4; DB 1; Length 12;
              Best Local Similarity 90.0%; Pred. No. 22;
              Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1170 CAACCTTGGC 1179
Db          3 CTACTTGGC 12
RESULT 36
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LOCUS      BQ591624
DEFINITION cDNA clone 024-017-P07-SP6 MPZ-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591624
VERSION   BQ591624.1 GI:26121207
KEYWORDS  EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 12)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 12 Std Error: 0.00
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              Seq primer: SP6; CATACGATTAGTGACACTATAG.
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              /lab_host="EMDH10B"
              /clone_lib="MPIZ-ADIS-024-storage root"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
              Query Match      0.4%; Score 8.4; DB 1; Length 12;
              Best Local Similarity 90.0%; Pred. No. 22;
              Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1170 CAACCTTGGC 1179
Db          3 CTACTTGGC 12
RESULT 36
BQ591624/c 12 bp mRNA linear EST 06-DEC-2002
LOCUS      BQ591624
DEFINITION cDNA clone 024-017-P07-SP6 MPZ-ADIS-024-storage root Beta vulgaris
ACCESSION BQ591624
VERSION   BQ591624.1 GI:26121207
KEYWORDS  EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
              1 (bases 1 to 12)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 12 Std Error: 0.00
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              Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES     Location/Qualifiers
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              /clone_lib="MPIZ-ADIS-024-storage root"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
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              Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"
              Query Match      0.4%; Score 8.4; DB 1; Length 12;
              Best Local Similarity 90.0%; Pred. No. 22;
              Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          1253 CCATCCCA 1262
Db          12 CCATCCCA 3
RESULT 37
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LOCUS      AQ050979
DEFINITION nbxb0004db1r CUGI Rice BAC Library Oryza sativa (japonica
              cultivar-group) genomic clone nbxb0004H22r, genomic survey
              sequence.
ACCESSION AQ050979
VERSION   AQ050979.2 GI:4501770
KEYWORDS  GSS.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 12)
              Wing,R.A. and Dean,R.A.
              A BAC End Sequencing Framework to Sequence the Rice Genome
              Unpublished (1998)
              On Mar 23, 1999 this sequence version replaced gi:3325284.
              Contact: Wing RA
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Tel: 864 656 7288
              Fax: 864 656 4293
              Email: rwing@clemson.edu
              Seq primer: GGAAACAGCTATGACCATG
              Class: BAC ends

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High quality sequence stop: 1.
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          /lab host="E. coli DH10B"
          /clone_lib="CUGI Rice BAC Library"
          /notes="vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
      Query Match          0.4%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 22;
      Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1015 GAAAAAGAGG 1024
      |||||
Db      11 GAAAAATAGG 2

RESULT 38
B07312
LOCUS      B07312      12 bp      DNA      linear      GSS      26-MAR-1997
DEFINITION      G360T3 MVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
ACCESSION      B07312.1      GI:1667053
VERSION      B07312.1
KEYWORDS      Trypanosoma brucei rhodesiense
SOURCE      Trypanosoma brucei rhodesiense
ORGANISM      Trypanosoma brucei rhodesiense
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE      1 (bases 1 to 12)
AUTHORS      El-Sayed,N.M.A. and Donelson,J.E.
TITILE      A survey of the Trypanosoma brucei rhodesiense genome using shotgun sequencing
JOURNAL      Mol. Biochem. Parasitol. 84 (2), 167-178 (1997)
MEDLINE      97237559
PUBMED      9084037
COMMENT      Other GSSs: G360T7
              Contact: El-Sayed NMA
              John Donelson's Laboratory
              Howard Hughes Medical Institute
              300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
              52242
              Tel: 319 335 6918
              Fax: 319 335 6764
              Email: neilsayed@vaxa.weeg.uiowa.edu
              Insert Length: 700 Std Error: 200.00
              Seq primer: T3 primer
              Class: shotgun.
              Location/Qualifiers
                1. .12
                  /organism="Trypanosoma brucei rhodesiense"
                  /mol_type="genomic DNA"
                  /sub_species="rhodesiense"
                  /db_xref="taxon:31286"
                  /clone="G360"
                  /dev stage="Bloodstream form"
                  /clone_lib="MVAT4 sheared genomic library"
                  /notes="vector: PCR-Script Amp SK(+) (Stratagene); Site_1: Srf I; Genomic DNA was isolated from a cloned population of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). For the shotgun library construction, the DNA was mechanically sheared to give a tight size distribution, then blunt-ended, with T4 DNA polymerase. Following dephosphorylation with Shrimp Alkaline Phosphatase, DNA fragments were cloned into the PCR-Script vector (Stratagene)."

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Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      301 CTGGAGCT 308
      1 CTGGAGCT 8

RESULT 40
CF277997
LOCUS      14ETL--03-L19.g1 Rice etiolated leaf plasmid cDNA library (14ETL) EST 14-AUG-2003
DEFINITION      Oryza sativa cDNA clone 14ETL--03-L19, mRNA sequence.
ACCESSION      CF277997.1 GI:33653383
VERSION      CF277997.1
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-L19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTT TTTT 1973
      1 TTTT TTTT 8

RESULT 41
CF301888/c
LOCUS      7LEAF--06-O17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--06-O17, mRNA sequence.
ACCESSION      CF301888
VERSION      CF301888.1 GI:33673649
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTT TTTT 1973
      1 TTTT TTTT 8

RESULT 42
CF302851/c
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION      CF302851.1 GI:33674612
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-L19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTT TTTT 1973
      1 TTTT TTTT 8

RESULT 43
CF302851/c
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION      CF302851.1 GI:33674612
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--06-O17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

```

```

TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-O17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1966 TTTT TTTT 1973
      1 TTTT TTTT 8

RESULT 44
CF302851/c
LOCUS      7LEAF--08-M07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza EST 15-AUG-2003
DEFINITION      sativa cDNA clone 7LEAF--08-M07, mRNA sequence.
ACCESSION      CF302851
VERSION      CF302851.1 GI:33674612
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-M07"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 TTTTTTTT 1973
DB 8 TTTTTTTT 1

RESULT 43
CF312818/c
LOCUS      8 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-L15, mRNA sequence.
ACCESSION  CF312818
VERSION     CF312818.1 GI:33684579
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE  1 (bases 1 to 8)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1..8
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF--08-L15"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

FEATURES             source
            1..8
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF--08-L15"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      0.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 TTTTTTTT 1973
DB 8 TTTTTTTT 1

RESULT 44
CF309109/c
LOCUS      9 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--03-C20, mRNA sequence.
ACCESSION  CF309109
VERSION     CF309109.1 GI:33680870
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Spermatophyta;

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Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1..9
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF--03-C20"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
            cDNA library (ABF)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 637 AGGAAGAA 644
DB 9 AGGAAGAA 2

RESULT 45
CF312817
LOCUS      9 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-L15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--08-L15, mRNA sequence.
ACCESSION  CF312817
VERSION     CF312817.1 GI:33684578
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            1..9
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="ABF--08-L15"
            /tissue_type="leaf"

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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
Db 1 TTTTTTTT 8

RESULT 46
CF318771
LOCUS
DEFINITION HD--09-A13.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa CDNA clone HD--09-A13, mRNA sequence.
ACCESSION CF318771
VERSION HD--09-A13
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-A13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
Db 1 TTTTTTTT 8

RESULT 47
CF330649
LOCUS
DEFINITION NACL--06-H06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa CDNA clone NACL--06-H06, mRNA sequence.
ACCESSION CF330649
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 9)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.4%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 TTTTTTTT 1973
Db 1 TTTTTTTT 8

RESULT 48
CF333615
LOCUS
DEFINITION JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa CDNA clone JMT--02-J09, mRNA sequence.
ACCESSION CF333615
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE Contact: Nahm B.H.
JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--09-A13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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source
1. .10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-J09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1309 GACACTGA 1316
Db 2 GACACTGA 9

RESULT 49
CA794390/c
LOCUS
DEFINITION
CA794390 10 bp mRNA linear EST 05-DEC-2002
Theobroma cacao Cac_BL_1340 5', mRNA sequence.
ACCESSION
CA794390
VERSION
CA794390.1 GI:26051466
KEYWORDS
EST.
SOURCE
Theobroma cacao (cacao)
ORGANISM
Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 10)
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
MEDLINE
12447539
PUBMED
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
FEATURES
Location/Qualifiers
1. .10
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 1340"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonado type
Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

Query Match      0.4%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 183 GGAAGCCC 190
Db 8 GGAAGCCC 1

RESULT 50
CF322692/c
LOCUS
DEFINITION
CF322692 11 bp mRNA linear EST 18-AUG-2003
HDN--01-M19_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa CDNA clone HDN--01-M19, mRNA
sequence.
ACCESSION
CF322692
VERSION
CF322692.1 GI:33793616
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1. .11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--01-M19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1236 AGCCCTCG 1243
Db 11 AGCCCTCG 4

RESULT 51
BG925521/c
LOCUS
DEFINITION
BG925521 12 bp mRNA linear EST 06-NOV-2001
HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG925521
VERSION
BG925521.1 GI:14320044
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathie, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

```

Lark.M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651
 MEDLINE
 PUBMED
 COMMENT
 Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-legsk.com
 Seq primer: T7.

FEATURES

source

1. .12
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HMC (Human Normal Cartilage)"
 /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
 Directional"

Query Match 0.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 78 GGAGGGGA 85
 |||||
 Db 12 GGAGGGGA 5

RESULT 52
 BQ587288
 LOCUS
 DEFINITION
 clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
 VERSION
 BQ587288.1 GI:26116870
 EST.
 Beta vulgaris
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 12)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 PUBMED
 COMMENT
 Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 12 Std Error: 0.00
 Plate: 10 row: G column: 19
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source

1. .12
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="RWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:185570"

/db_xref="taxon:161934"
 /clone="024-010-G19"
 /tissue_type="leaf"
 /lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TTTTTCCT 1690

|||||
 Db 1 TTTTTCCT 8

RESULT 53

BQ587706

LOCUS

DEFINITION

clone 024-010-G19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA

VERSION

BQ587706.1

EST.

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 12)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 PUBMED
 COMMENT
 Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 12 Std Error: 0.00
 Plate: 10 row: G column: 19
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source

1. .12
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 /cultivar="RWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:185160"
 /db_xref="taxon:161934"
 /clone="024-010-G19"
 /tissue_type="leaf"
 /lab_host="EMDH10B"
 /clone_lib="MP1Z-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:

SP6-SALI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1683 TTTTCTCT 1690
Db 1 TTTTCTCT 8

RESULT 54
BQ595423
LOCUS
DEFINITION BQ595423 13 bp mRNA linear EST 06-DEC-2002
E012693-024-022-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-N20 5-PRIME, mRNA sequence.

ACCESSION BQ595423.1 GI:26125006
VERSION
KEYWORDS
SOURCE
ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL
MEDLINE
PUBMED
COMMENT

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 22 row: N column: 20
Seq primer: SP6; CATACGATTTAGTGACACTATAG.

FEATURES
source

1. .13
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line)"
/db_xref="GABI:191428"
/db_xref="taxon:161934"
/clone="024-022-N20"
/tissue_type="developing root"
/lab_host="EMPH108"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:

SP6-SALI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.4%; Score 8; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GAGAAATTC 57
Db 1 GAGAAATTC 8

RESULT 55
BQ927412

LOCUS
DEFINITION

BQ927412 11 bp mRNA linear EST 06-NOV-2001
HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BQ927412
VERSION BQ927412.1 GI:14321935
KEYWORDS
SOURCE

Homo sapiens (human)
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sath, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.

TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-legsk.com
Seq primer: 17.

Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="vector: pSPORT 1; Site 1: SalI; Site 2: NotI;
Directional"

FEATURES
source

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 841 CTACCCCGAGAT 851
Db 1 CTACCCCGAGCT 11

RESULT 56
BQ927896/c

LOCUS
DEFINITION

BQ927896 11 bp mRNA linear EST 06-NOV-2001
HNC45-1-D11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BQ927896
VERSION BQ927896.1 GI:14322419
KEYWORDS
SOURCE

Homo sapiens (human)
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sath, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.

TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and

```

JOURNAL Osteoarthritic cartilage cDNA libraries
MEDLINE Osteoarthr. Cartil. 9 (7), 641-653 (2001)
PUBMED 21482651
COMMENT 11597177
Contact: Sanjay Kumar
UW2109 GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7

FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1011 ACCTGAAAAAG 1021
|||||
Db 11 ACCTGCAACG 1

RESULT 57
BM395997 11 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-15-D12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395997
VERSION 1
KEYWORDS
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 11)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 877 TCAGGCACAC 887
|||||
Db 11 TCCGGCGCCAC 1

RESULT 59
BQ585943 11 bp mRNA linear EST 06-DRC-2002
LOCUS E012531-024-014-K17-SP6 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-014-K17 5-PRIME, mRNA sequence.
ACCESSION BQ585943
VERSION 1
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 11)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drugowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ

Query Match 0.4%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GTTGGCGTGA 1369

```

Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@piz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
 Plate: 14 row: K column: 17
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source
 1. .11
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:186918"
 /db_xref="taxon:161934"
 /clone="024-014-K17"
 /tissue_type="leaf"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-leaf"
 /note="Vector: PCWVSPOR76; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinvanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1239 CCTCGCGTCGCG 1249
 |||||
 Db 11 CCACGCGTCGCG 1

RESULT 60
 BQ593914/c
 LOCUS
 DEFINITION S015507-024-025-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 CDNA clone 024-025-N20 5-PRIME, mRNA sequence.
 ACCESSION BQ593914
 VERSION BQ593914.1 GI:26123497
 KEYWORDS EST.
 SOURCE Beta vulgaris

ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
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 Seq primer: SP6; CATACGATTAGTGACACTATAG.
 Location/Qualifiers
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 /organism="Beta vulgaris"

/mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:192937"
 /db_xref="taxon:161934"
 /clone="024-025-N20"
 /tissue_type="developing root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-developing root"
 /note="Vector: PCWVSPOR76; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinvanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1238 CCTCGCGTCGCG 1248
 |||||
 Db 11 CCACGCGTCGCG 1

RESULT 61
 BQ238234
 LOCUS
 DEFINITION Ds01_01e11 R Ds01 AAFQ ECORC cold stressed Flixweed seedlings
 Descurainia sophia cDNA clone Ds01_01e11, mRNA sequence.
 ACCESSION BQ238234
 VERSION BQ238234.1 GI:22750059
 KEYWORDS EST.
 SOURCE Descurainia sophia

ORGANISM Descurainia sophia
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
 1 (bases 1 to 11)
 Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Spott,D. and Tinker,N.A.
 TITLE Expressed Sequence Tags from Cold-Stressed Descurainia sophia Seedlings

Unpublished (2001)
 Contact: Singh,J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@agr.ca.

Location/Qualifiers
 1. .11
 /organism="Descurainia sophia"
 /mol_type="mRNA"
 /db_xref="taxon:89411"
 /clone="Ds01_01e11"
 /tissue_type="leaf, stem"
 /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
 /clone_lib="Ds01 AAFQ ECORC cold stressed Flixweed seedlings"
 9s

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 20°C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20°C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."

FEATURES

source
 1. .11
 /organism="Beta vulgaris"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 371 AGAGAGATAGT 381
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 Db 1 AGAGAACTAGT 11

RESULT 62
 CF323154 11 bp mRNA linear EST 18-AUG-2003
 LOCUS HDN-03-B04.g1 OshDAC1-overexpressing transgenic rice lambda phage
 DEFINITION cDNA library II (HDN) Oryza sativa cDNA clone HDN-03-B04, mRNA
 sequence.

ACCESSION CF323154 GI:33794534
 VERSION CF323154.1
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 11)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.

FEATURES
 source
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 /organism="Oryza sativa"
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 /cultivar="Nackdong"
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 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOL8"
 /clone_lib="OshDAC1-overexpressing transgenic rice lambda
 phage cDNA library II (HDN)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
 5' end with EcoRI and 3' end with XhoI site. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 GCACGAGGTG 837
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 Db 1 GCACGAGGGTG 11

RESULT 63
 CF543031 11 bp mRNA linear EST 22-SEP-2003
 LOCUS S01532-024-030-P02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-030-P02 5-PRIME, mRNA sequence.

ACCESSION CF543031 GI:34891471
 VERSION CF543031.1
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189
 MEDLINE 12472698
 PUBMED
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
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 Seq primer: SP6.

FEATURES
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 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:936732"
 /db_xref="taxon:161934"
 /clone="024-030-P02"
 /tissue_type="leaf"
 /lab_host="EMPH10B"
 /clone_lib="MP1Z-ADIS-024-leaf"
 /note="Vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1092 CACCCCCCACC 1102
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 Db 11 CCCCCCCCCC 1

RESULT 64
 BQ587870/c 12 bp mRNA linear EST 06-DEC-2002
 LOCUS S013708-024-009-P23-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-009-P23 5-PRIME, mRNA sequence.

ACCESSION BQ587870 GI:26117452
 VERSION BQ587870.1
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)
 AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189
 MEDLINE

```

PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 9 row: P column: 23
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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                /db_xref="taxon:161934"
                /clone="024-020-P03"
                /tissue_type="storage root"
                /lab_host="EMDH108"
                /clone_lib="MPIZ-ADIS-024-storage root"
                /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
            Query Match 0.4%; Score 7.8; DB 1; Length 12;
            Best Local Similarity 81.8%; Pred. No. 45;
            Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
        QY 605 GCACAGTGCAC 615
        Db 11 GCAAGTGCAC 1
        RESULT 66
        LOCUS B07312/c 12 bp DNA linear GSS 26-MAR-1997
        DEFINITION B07312 MVAT4 sheared genomic library trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
        ACCESSION B07312.1 GI:1667053
        VERSION B07312
        KEYWORDS GSS.
        SOURCE Trypanosoma brucei rhodesiense
        ORGANISM Trypanosoma brucei rhodesiense
        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
        REFERENCE 1 (bases 1 to 12)
        AUTHORS El-Sayed,N.M.A. and Donelson,J.E.
        TITLE A survey of the Trypanosoma brucei rhodesiense genome using shotgun sequencing
        JOURNAL Mol. Biochem. Parasitol. 84 (2), 167-178 (1997)
        MEDLINE 97237559
        PUBMED 9084037
        COMMENT Other_GSSs: G360T7
        Contact: El-Sayed NMA
        John Donelson's Laboratory
        Howard Hughes Medical Institute
        300 EMBB, Dept. of Biochemistry, University of Iowa, Iowa City, IA 52242
        Tel: 319 335 6918
        Fax: 319 335 6764
        Email: nelsayed@evax.wiwi.uiowa.edu
        Insert Length: 700 Std Error: 200.00
        Seq primer: T3 primer
        Class: shotgun.
FEATURES
    source
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            1..12
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                /clone="G360"
                /dev_stage="Bloodstream form"
                /clone_lib="MVAT4 sheared genomic library"
                /note="Vector: PCR-Script Amp SK(+) (Stratagene); Site_1:

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Srf I; Genomic DNA was isolated from a cloned population of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). For the shotgun library construction, the DNA was mechanically sheared to give a tight size distribution, then blunt-ended with T4 DNA polymerase. Following dephosphorylation with Shrimp Alkaline Phosphatase, DNA fragments were cloned into the PCR-Script vector (Stratagene)."

Query Match 0.4%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1403 ACAGATCGAT 1413
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Db 12 ACGGATCGAT 2

RESULT 67
CNS06ESN/ c
LOCUS
DEFINITION CNS06ESN 9 bp DNA linear GSS 17-JUN-2001
T3 end of clone AROAA018H04 of library AROAA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION
VERSION AL394689
KEYWORDS
SOURCE AL394689.1 GI:12145788
ORGANISM
Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.
REFERENCE
1 (bases 1 to 9)
Souciet, J.-L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 9)
de Montigny, J., Straub, M., Potier, S., Tekala, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
Zygosaccharomyces rouxii
FEBS Lett. 487 (1), 52-55 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
JOURNAL
TITLE
COMMENT
3 (bases 1 to 9)
Genoscope.
Direct Submission
Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES
source
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Location/Qualifiers
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/clone="AROAA018H04"
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Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 904 GTCAATTT 911
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Db 9 GTCAATTT 2

RESULT 68
CF307276/c
LOCUS
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HDA1--06-D23.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-D23, mRNA
sequence.
ACCESSION
VERSION CF307276.1 GI:33679037
KEYWORDS
SOURCE CF307276
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhn@gbio.com, bnhn@gbio.myongji.ac.kr.

FEATURES
source
1..9
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1--06-D23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
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Db 9 GTGCCACCT 1

RESULT 69
CF307431/c
LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDA1--06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-K23, mRNA
sequence.
ACCESSION
VERSION CF307431
KEYWORDS
SOURCE CF307431
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhn@gbio.com, bnhn@gbio.myongji.ac.kr.

FEATURES
source
1..9
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1--06-D23"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1124 GTTCCACCT 1132
||| |||||
Db 9 GTGCCACCT 1

RESULT 69
CF307431/c
LOCUS
DEFINITION CF307431 9 bp mRNA linear EST 15-AUG-2003
HDA1--06-K23.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--06-K23, mRNA
sequence.
ACCESSION
VERSION CF307431
KEYWORDS
SOURCE CF307431
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhn@gbio.com, bnhn@gbio.myongji.ac.kr.

FEATURES
source
1..9
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1--06-D23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

```

VERSION      CF307431.1  GI:33679192
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 9)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Gyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
             1..9
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="HDAL-06-K23"
             /tissue_type="callus"
             /dev_stage="proliferated callus on 2N6 media for 2 weeks"
             /lab_host="E.coli SOLR"
             /clone_lib="OshDAC1-overexpressing transgenic rice lambda
             phage cDNA library I (HDAL)"
             /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
             XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
             was inserted into lambda Uni-ZAP XR vector at 5' end with
             EcoRI and 3' end with XhoI site. mRNA was derived from
             rice Histone Deacetylase overexpression line."
             Query Match      0.3%; Score 7.4; DB 1; Length 9;
             Best Local Similarity 88.9%; Pred. No. 1.1e+02;
             Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           1124 GTTCCACCT 1132
Db           1124 GTTCCACCT 1132
             1124 GTTCCACCT 1132
             9 GTGCCACCT 1

RESULT 70
CAB50813
LOCUS        D06G10_G10_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION   cDNA clone D06G10 5', mRNA sequence.
ACCESSION    CAB50813
VERSION      CAB50813.1  GI:33387606
KEYWORDS     EST.
SOURCE       Glycine max (soybean)
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
             Glycine.
REFERENCE    1 (bases 1 to 9)
AUTHORS      Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE        Analysis of expressed sequence tags from roots of resistant soybean
             infected by the soybean cyst nematode
JOURNAL      Unpublished (2002)
COMMENT      Contact: Alkharouf, N.W.
             Soybean Genomics and Improvement Laboratory (SGIL)
             US Department of Agriculture (USDA), ARS, PSI
             Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
             USA
             Tel: 301 504 5750
             Fax: 301 504 5728
             Email: alkharouf@ba.ars.usda.gov.

```

```

FEATURES     Location/Qualifiers
             1..9
             /organism="Glycine max"
             /mol_type="mRNA"
             /cultivar="Peking"
             /db_xref="taxon:3847"
             /clone="D06G10"
             /tissue_type="Roots"
             /dev_stage="Seedlings"
             /clone_lib="cDNA Peking library 2, 4 day SCN3"
             /note="Vector: pBluescript SK-; cDNA clones from mRNA
             extracted from Peking roots 2 and 4 days past invasion."
             Query Match      0.3%; Score 7.4; DB 1; Length 9;
             Best Local Similarity 88.9%; Pred. No. 1.1e+02;
             Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           992 TTGTTTGTG 1000
Db           992 TTGTTTGTG 1000
             992 TTGTTTGTG 1000
             1 TTGTTTGTG 9

RESULT 71
CF313414
LOCUS        HD--01-I15.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION   library (HD) Oryza sativa cDNA clone HD--01-I15, mRNA sequence.
ACCESSION    CF313414
VERSION      CF313414.1  GI:33685175
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 9)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Gyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
             1..9
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="HD--01-I15"
             /tissue_type="callus"
             /dev_stage="proliferated callus on 2N6 media for 2 weeks"
             /lab_host="E.coli DH10B"
             /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
             cDNA library (HD)"
             /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
             treated with ABA(20um) for 1hr. Oligo-capped mRNA was
             reverse transcribed and then used for PCR. mRNA was
             derived from rice Histone Deacetylase overexpression
             line."
             Query Match      0.3%; Score 7.4; DB 1; Length 9;
             Best Local Similarity 88.9%; Pred. No. 1.1e+02;
             Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY           817 AGCTTGAG 825
Db           817 AGCTTGAG 825
             817 AGCTTGAG 825
             1 AGACTGGAG 9

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RESULT 72
CF313414/c
LOCUS
DEFINITION HD--01-I15.bi OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-I15, mRNA sequence.

ACCESSION CF313414
VERSION CF313414.1 GI:33685175
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-I15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pC4-TOPO; Site:1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 CTCGAGTCT 1090
Db 9 CTCGAGTCT 1

RESULT 73
CF323490
LOCUS
DEFINITION HDN--03-P21.g1 OshDACL1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA sequence.

ACCESSION CF323490
VERSION CF323490.1 GI:33795236
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1082 CTCGAGTCT 1090
Db 9 CTCGAGTCT 1

RESULT 73
CF323490
LOCUS
DEFINITION HDN--03-P21.g1 OshDACL1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA sequence.

ACCESSION CF323490
VERSION CF323490.1 GI:33795236
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--03-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOIR"
/clone_lib="OshDACL1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site:1: EcoRI; Site:2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAGT 835

Db 1 GCACGAGT 9

RESULT 74

CF307092

LOCUS

DEFINITION

HD1--05-I14.g1 OshDACL1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa cDNA clone HDA1--05-I14, mRNA sequence.

ACCESSION

CF307092

VERSION

CF307092.1 GI:33678853

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1--05-I14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOIR"
/clone_lib="OshDACL1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"
/note="Vector: pBluescript SK(+); Site:1: EcoRI; Site:2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1524 CGTGCTCG 1532
||| |||||
Db 1 CGAGCTCG 9

RESULT 75
CF322585
LOCUS
DEFINITION HDN--01-H22.g1 OshDAC1-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa cDNA clone HDN--01-H22, mRNA
sequence.

ACCESSION CF322585
VERSION CF322585.1 GI:33793411
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage CDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1443 GCACGAGGC 1451
||| |||||
Db 1 GCACGAGGC 9

RESULT 76
CF322585/c
LOCUS
DEFINITION HDN--01-H22.g1 OshDAC1-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa cDNA clone HDN--01-H22, mRNA
sequence.

ACCESSION CF322585

CF322585.1 GI:33793411

EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--01-H22"
/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OshDAC1-overexpressing transgenic rice lambda

phage CDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1877 GCCTCATGC 1885

||| |||||

Db 9 GCCTCATGC 1

RESULT 77

CF325534

LOCUS

DEFINITION

JMT1--03-H24.g1 AtJMT-overexpressing transgenic rice lambda phage
CDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-H24, mRNA
sequence.

ACCESSION CF325534

VERSION CF325534.1 GI:33799350

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 9)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers


```

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES
source
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1--03-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1877 GCTCATGC 1885
|||||
Db 9 GCTCGTGC 1

RESULT 81
BG925375
LOCUS HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG925375.1 GI:14319898
VERSION BG925375.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@glaxo.com
Seq primer: T7.
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source
1..10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT1--03-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JMT1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1240 CTCGCCTCC 1248
|||||
Db 1 CTCGCATCC 9

RESULT 82
BM396082
LOCUS 5009-0-16-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396082.1 GI:18196135
VERSION BM396082
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 10)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1334 ACCCGCTGG 1342
|||||
Db 2 ACCGCGTGG 10

RESULT 83
BM396082/c
LOCUS 5009-0-16-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396082
VERSION BM396082.1 GI:18196135
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

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```

REFERENCE
1 (bases 1 to 10)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match
Best Local Similarity 0.3%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 621 CACCGGTG 629
|||||
DB 9 CACCGGTG 1

RESULT 84
BQ789997/c
LOCUS
DEFINITION
hage005ad02 Heterobasidion annosum - Scots pine infection stage
(HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
annosum cDNA clone hage005ad02, mRNA sequence.
ACCESSION
BQ789997
VERSION
BQ789997.1 GI:22004959
KEYWORDS
EST.
SOURCE
Pinus sylvestris/Heterobasidion annosum
Pinus sylvestris/Heterobasidion annosum
Eukaryota; mixed EST libraries.
ORGANISM
1 (bases 1 to 10)
REFERENCE
Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
Selected Expressed sequence tags of cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
Unpublished (2001)
JOURNAL
COMMENT
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
1..10
/organism="Pinus sylvestris/Heterobasidion annosum"
/mol_type="mRNA"
/db_xref="taxon:169015"
/clone_lib="hage005ad02"
/dev_stage="Seedling roots of scots pine were infected for
6 days with H. annosum"
/clone_lib="Heterobasidion annosum - Scots pine infection
stage (HAGE) subtraction cDNA library"
/note="Vector: pT-Adv; Site:1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots pine
roots infected for 6-days with mycelia of Heterobasidion
annosum (FP5)."

Query Match
Best Local Similarity 0.3%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 621 CACCGGTG 629
|||||
DB 9 CACCGGTG 1

RESULT 84
BQ789997/c
LOCUS
DEFINITION
hage005ad02 Heterobasidion annosum - Scots pine infection stage
(HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
annosum cDNA clone hage005ad02, mRNA sequence.
ACCESSION
BQ789997
VERSION
BQ789997.1 GI:22004959
KEYWORDS
EST.
SOURCE
Pinus sylvestris/Heterobasidion annosum
Pinus sylvestris/Heterobasidion annosum
Eukaryota; mixed EST libraries.
ORGANISM
1 (bases 1 to 10)
REFERENCE
Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
Selected Expressed sequence tags of cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
Unpublished (2001)
JOURNAL
COMMENT
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
1..10
/organism="Pinus sylvestris/Heterobasidion annosum"
/mol_type="mRNA"
/db_xref="taxon:169015"
/clone_lib="hage005ad02"
/dev_stage="Seedling roots of scots pine were infected for
6 days with H. annosum"
/clone_lib="Heterobasidion annosum - Scots pine infection
stage (HAGE) subtraction cDNA library"
/note="Vector: pT-Adv; Site:1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots pine
roots infected for 6-days with mycelia of Heterobasidion
annosum (FP5)."

```

```

Query Match
Best Local Similarity 0.3%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1206 CTATCAGGG 1214
|||||
DB 9 CTATCAGAG 1

RESULT 85
CF311011
LOCUS
DEFINITION
ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.
ACCESSION
CF311011
VERSION
CF311011.1 GI:33682772
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone_lib="ABF--06-B02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 0.3%; Score 7.4; DB 1; Length 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 934 CTCCTCTTC 942
|||||
DB 2 CTCCTCTTC 10

RESULT 86
CF311011/c
LOCUS
DEFINITION
ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-B02, mRNA sequence.
ACCESSION
CF311011
VERSION
CF311011.1 GI:33682772
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 10)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Source
 1..10
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF-06-B02"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 76 GAGGAGGG 84
 |||||
 Db 10 GAGGAGGAG 2

RESULT 87
 CA794390
 LOCUS
 DEFINITION
 Theobroma cacao cDNA clone Cac_BL_1340 5', mRNA sequence.

ACCESSION
 CA794390
 VERSION
 CA794390.1 GI:26051466
 KEYWORDS
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 1 (bases 1 to 10)
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
 Retzel, E.R. and Jones, C.A.

TITLE
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties

JOURNAL
 MEDLINE
 PUBLISHED
 2237596
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com

Seq primer: T3.
 Location/Qualifiers
 1..10
 /organism="Theobroma cacao"
 /mol_type="mRNA"

FEATURES

Source
 1..10
 /organism="Theobroma cacao"
 /mol_type="mRNA"

/strain="Amelonado type"
 /db_xref="taxon:3641"
 /clone="Cac BL 1340"
 /tissue_type="Mature leaf and mature bean"
 /cell_type="Whole organ"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac BL (Bean and Leaf from Amelonado type
 Cacao)"

/note="vector: pBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

Query Match 0.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1548 GGGCTGCCT 1556
 |||||
 Db 1 GGGCTTCCT 9

RESULT 88

BM395226
 LOCUS

DEFINITION
 50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION
 BM395226

VERSION
 BM395226.1 GI:18195279

KEYWORDS
 EST.

SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 11)

AUTHORS
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
 Frankel, J. and Klobutcher, L.

TITLE
 EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL
 Unpublished (2002)

COMMENT
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source
 1..11
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 0.3%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1570 GAGGCGCTT 1578
 |||||
 Db 3 GTGGCGCTT 11

RESULT 89

BH169696/c
 LOCUS

DEFINITION
 SALK_001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_001766, genomic survey sequence.

ACCESSION
 BH169696

VERSION
 BH169696.1 GI:15905071

BH169696 12 bp DNA linear GSS 03-OCT-2001
 SALK_001766 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_001766, genomic survey sequence.

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 12)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmermann,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

FEATURES

source
1..12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"

/db_xref="taxon:3702"
/clone="SALK 001766"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 0.3%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1577 TTGGGGCC 1585
Db 10 TTGGGGCC 2

RESULT 90
BQ591624 12 bp mRNA linear EST 06-DEC-2002
LOCUS E012618-024-017-P07-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION CDNA clone 024-017-P07 5-PRIME, mRNA sequence.
ACCESSION BQ591624
VERSION BQ591624.1 GI:26121207
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 12)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Hrsgowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE
PUBMED 22362189
12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

FEATURES

source

1..12
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"

/db_xref="taxon:161934"

/db_xref="GABI:188488"

/clone="024-017-P07"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.3%; Score 7.4; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 996 TTGTGGGAA 1004
Db 1 TTTTGGGAA 9

RESULT 91

CF339091/c

LOCUS CF339091 8 bp mRNA linear EST 18-AUG-2003

DEFINITION RCL1--03-M05.g1 Regenerated callus lambda phage cDNA library (RCL1)

ORYZA sativa cDNA clone RCL1--03-M05, mRNA sequence.

ACCESSION CF339091

VERSION CF339091.1 GI:33826564

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-M05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library

```

(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match      0.3%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 AGCTCCA 1147
Db 8 AGCTCCA 2

RESULT 92
CF295648
LOCUS
DEFINITION      8 bp mRNA linear EST 14-AUG-2003
sativa cDNA clone 30DGS--05-K23, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-K23"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 ATATACC 325
Db 2 ATATACC 8

RESULT 93
CF921494
LOCUS
DEFINITION      8 bp mRNA linear EST 05-NOV-2003
gmhRw3-10_B07_1_061 Soybean root hair subtracted cDNA library
gmhRw3 Glycine_max cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS      Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
TITLE      Expressed sequence tags from soybean root hair subtractive cDNA
library
JOURNAL
COMMENT      Unpublished (2003)
Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
Tel: 573-884-4752
Fax: 573-882-0588
Email: stacey@missouri.edu
Single pass sequence
Seq primer: T7
Location/Qualifiers
1. .8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmhRw3"
/note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

Query Match      0.3%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1973 TGTGTTT 1979
Db 2 TGTGTTT 8

RESULT 94
CA851350/c
LOCUS
DEFINITION      8 bp mRNA linear EST 01-AUG-2003
cDNA clone D12G08 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS      Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE      Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
JOURNAL
COMMENT      Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1. .8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"

```

```

/db_xref="taxon:3847"
/clone="D12G08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 7; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1889 TTTTGGGT 1896
      |||||
Db 8 TTTTGGGT 1

RESULT 95
CF313731/c
LOCUS
DEFINITION HD--01-P12.gi OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
ACCESSION CF313731
VERSION CF313731.1 GI:33685492
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-P12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E. coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 533 AAAACCA 539
      |||||
Db 8 AAAACCA 2

RESULT 96
CA851674/c
LOCUS
DEFINITION D16C10_F22_05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max

```

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cDNA clone D16C10 5', mRNA sequence.
CA851674 GI:33388467
VERSION CA851674.1 GI:33388467
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
source
1..9
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D16C10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 CTTTGT 2138
      |||||
Db 7 CTTTGT 1

RESULT 97
BM396043
LOCUS
DEFINITION 5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396043
VERSION BM396043.1 GI:18196096
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 10)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: F3.
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"

FEATURES
source

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/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 477 CCGGGG 483
Db 2 CCGGGG 8

RESULT 98
BM396043/c
LOCUS      10 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM396043
VERSION    BM396043.1 GI:18196096
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
REFERENCE  1 (bases 1 to 10)
AUTHORS   Frankel,J., and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1154 CCCCCG 1160
Db 9 CCCCCG 3

RESULT 99
CF323895
LOCUS      10 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--05-A22-g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
sequence.
ACCESSION  CF323895
VERSION    CF323895.1 GI:33796055
SOURCE     Oryza sativa
ORGANISM   Oryza sativa

/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 GCCCGAG 123
Db 1 GCCCGAG 7

RESULT 100
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LOCUS      10 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--05-A22-g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
sequence.
ACCESSION  CF323895
VERSION    CF323895.1 GI:33796055
SOURCE     Oryza sativa
ORGANISM   Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--05-A22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli SOLR"
/clone_lib="OsHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 GCCCGAG 123
Db 1 GCCCGAG 7

RESULT 100
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LOCUS      10 bp mRNA linear EST 18-AUG-2003
DEFINITION HDN--05-A22-g1 OsHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA
sequence.
ACCESSION  CF323895
VERSION    CF323895.1 GI:33796055
SOURCE     Oryza sativa
ORGANISM   Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 10)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..10
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"

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/db_xref="taxon:4530"
/clone="HDN--05-A22"
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/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluecript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

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Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1237 GCCCTCG 1243
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DB 10 GCCCTCG 4

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RESULT 101
CF336905
LOCUS JMT--07-C04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--07-C04, mRNA sequence.
ACCESSION CF336905
VERSION CF336905.1 GI:33822181
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

```

```

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongwi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
source
location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-C04"
/tissue_type="Leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pC4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Query Match      0.3%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1017 AAAAGAG 1023
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DB 1 AAAAGAG 7

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RESULT 102
BM395228
LOCUS BM395228
DEFINITION 50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395228
VERSION BM395228.1 GI:18195281
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila

```

```

REFERENCE
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

```

```

FEATURES
source
location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK4; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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```

Query Match      0.3%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1352 TGCCCCC 1358
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DB 3 TGCCCCC 9

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```

RESULT 103
BG927412/C
LOCUS BG927412
DEFINITION HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION BG927412
VERSION BG927412.1 GI:14321935
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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```

REFERENCE
AUTHORS Kumar,S., Connot,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sache,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

```

```

JOURNAL Osteoarthritis. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598

```

RESULT 105

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .12

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-K01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 7; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 GTCAGGT 590

Db 9 GTCAGGT 3

RESULT 107

BG925375/c

LOCUS

DEFINITION HNC5-1-A9.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION

BG925375

VERSION

BG925375.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Kumar, S., Connor, J.R., Dadds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lark, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteochondral cartilage cDNA libraries

Osteochondr. Cartil. 9 (7), 641-653 (2001)

21482651

PUBMED

11597177

CONTACT: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: 17.

Location/Qualifiers

1. .10

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

/clone_lib="HNC (Human Normal Cartilage)"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.3%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 46;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 77 AGGAGGGGAG 86

Db 10 AGGATCGGAG 1

RESULT 108

CF333615/c

LOCUS

DEFINITION

JMT--02-J09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--02-J09, mRNA sequence.

ACCESSION

CF333615

VERSION

CF333615.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 10)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. .10

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--02-J09"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.3%; Score 6.8; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 46;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 380 GTGTGTGTCC 389

Db 10 GTCACTGTCC 1

RESULT 109

CF336905/c

LOCUS

DEFINITION

JMT--07-C04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--07-C04, mRNA sequence.

ACCESSION

CF336905

VERSION

CF336905.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 10)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. .11
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-C04"
/tissue type="leaf"
/dev stages="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="ATJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 594 GATCTCTCTCT 603

Db 10 GAACCTCTTTT 1

RESULT 110

BQ590709
LOCUS E012597-024-018-024-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-018-024 5-PRIME, mRNA sequence.
ACCESSION BQ590709
VERSION BQ590709.1 GI:26120292
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 11)
Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Email: weishaar@mpiz-koeln.mpg.de
Fax: 00492215062851
Insert Length: 11 Std Error: 0.00
Plate: 18 row: 0 column: 24
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source
1. .11
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189410"

/db_xref="taxon:161934"
/clone="024-018-024"
/tissue type="storage root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-SPRime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1301 AGAGCCTAGA 1310

Db 1 AGAGCTTTGA 10

RESULT 111

CF322692
LOCUS HDN--01-M19-g1 OshDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-M19, mRNA
sequence.
ACCESSION CF322692
VERSION CF322692.1 GI:33793616
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. .11
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--01-M19"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab host="E.coli SOLR"
/clone lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.8; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1494 GCGGAGGCC 1503
||| |||||
Db 1 GCACGAGGC 10

RESULT 112
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
ACCESSION
A0050979
VERSION
nbxb0004d11r CUGI Rice BAC Library Oryza sativa (japonica
KEYWORDS
cultivar-group) genomic clone nbxb0004H22r, genomic survey
SOURCE
GSS.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 12)
REFERENCE
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
JOURNAL
On Mar 23, 1999 this sequence version replaced gi:3325284.
COMMENT
Contact: Wing RA
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..12
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbxb0004H22r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36,864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation of a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
Query Match 0.3%; Score 6.8; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 451 ACCTACTGTG 460
|||||
Db 1 ACCTATTTT 10

RESULT 114
LOCUS
DEFINITION
Theobroma cacao (cacao)
ACCESSION
CA798290
VERSION
GI:26055376
KEYWORDS
Theobroma cacao (cacao)
SOURCE
Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids 1; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 14)
REFERENCE
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao

```

```

RESULT 113
LOCUS
DEFINITION
SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_003378, genomic survey sequence.
ACCESSION
BH170808
VERSION
BH170808.1 GI:15906490
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids 1; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 13)
REFERENCE
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmermann, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
JOURNAL
Contact: Joseph R. Ecker
COMMENT
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..13
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_003378"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
Query Match 0.3%; Score 6.8; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 288 GCCGCTGGTG 297
|||||
Db 1 GCCGGCGGTG 10

RESULT 114
LOCUS
DEFINITION
Cac BL_611 Cac BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_611 5', mRNA sequence.
ACCESSION
CA798290
VERSION
GI:26055376
KEYWORDS
Theobroma cacao (cacao)
SOURCE
Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids 1; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 14)
REFERENCE
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao

```

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L.) varieties
Planta 216 (2), 255-264 (2002)
22337596
12447539
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
Location/Qualifiers
1. .14
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 611"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonado type Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."

Query Match 0.3%; Score 6.8; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1020 AGAGGGGAG 1029
Db 10 ATAGGGGAG 1

RESULT 115
CF305141
LOCUS
DEFINITION
ABF1--06-009, g1 ABF3-overexpressing transgenic rice lambda phage
cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-009, mRNA
sequence.
ACCESSION
CF305141
VERSION
CF305141.1 GI:33676902
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF1--06-009"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834
Db 1 GCACGAG 8

RESULT 116
CF305141/c
LOCUS
DEFINITION
ABF1--06-009, g1 ABF3-overexpressing transgenic rice lambda phage
cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-009, mRNA
sequence.
ACCESSION
CF305141
VERSION
CF305141.1 GI:33676902
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF1--06-009"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 117
CF306116
LOCUS
DEFINITION
ABF1--06-009, g1 ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1) Oryza sativa cDNA clone ABF1--06-009, mRNA
sequence.
ACCESSION
CF306116
VERSION
CF306116.1 GI:33676902
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 8)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF1--06-009"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

DEFINITION HDAL--02-L22-g1 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA sequence.

ACCESSION CF306116

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..8

Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDAL--02-L22"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 0.3%; Score 6.4; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834

|||||

Db 1 GCACGAGG 8

RESULT 118

CF306116/c

LOCUS

DEFINITION HDAL--02-L22-g1 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA sequence.

ACCESSION CF306116

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea

Query Match

Best Local Similarity 0.3%; Score 6.4; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834

|||||

Db 1 GCACGAGG 8

RESULT 118

CF306116/c

LOCUS

DEFINITION HDAL--02-L22-g1 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA sequence.

ACCESSION CF306116

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea

Query Match

Best Local Similarity 0.3%; Score 6.4; DB 1; Length 8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834

|||||

Db 1 GCACGAGG 8

RESULT 118

CF306116/c

LOCUS

DEFINITION HDAL--02-L22-g1 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L22, mRNA sequence.

ACCESSION CF306116

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 8)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..8

Location/Qualifiers

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/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 119

CF306762

LOCUS

DEFINITION HDAL--04-M13-g1 OSHDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--04-M13, mRNA sequence.

ACCESSION CF306762

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

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ACCESSION CF306762

VERSION

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ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

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ACCESSION CF306762

VERSION

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QY 1878 CCTCATGC 1885

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ACCESSION CF306762

VERSION

KEYWORDS

SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryza.

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
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Db      1 GCACGAGG 8

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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FEATURES
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was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
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RESULT 121
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ACCESSION CF322514
VERSION CF322514.1 GI:33793267
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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JOURNAL Unpublished (2003)
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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rice Histone Deacetylase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
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RESULT 122
CF322514/c
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ACCESSION CF322514
VERSION CF322514.1 GI:33793267
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Ehrhartoideae; Oryzeae; Oryza.
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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression
line."

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ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 8)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db      1 GCACGAGG 8

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LOCUS
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          cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-E13, mRNA
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ACCESSION CF322514
VERSION CF322514.1 GI:33793267
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Query Match 0.3%; Score 6.4; DB 1; Length 8;
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cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-K24, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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RESULT 123
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LOCUS
DEFINITION
HDN--01-K24_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-K24, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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AUTHORS
TITLE
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COMMENT
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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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line."

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RESULT 125
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sequence.
ACCESSION
VERSION
KEYWORDS
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ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
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Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 8 CCTCGTGC 1

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HDN--05-A16_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.
ACCESSION
VERSION
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Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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LOCUS
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HDN--05-A16_g1 OshDAC1-overexpressing transgenic rice lambda phage
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sequence.
ACCESSION
VERSION
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ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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AUTHORS
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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Db 1 GCACGAGG 8

RESULT 124
CF322653/c

LOCUS
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ACCESSION
VERSION
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 CCTCATGC 1885
|||||
DB 8 CCTCGTGC 1

RESULT 125
CF323889
LOCUS
DEFINITION

HDN--05-A16_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Email: bhnahm@bio.myongji.ac.kr.

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5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 CCTCATGC 1885
|||||
DB 8 CCTCGTGC 1

RESULT 125
CF323889
LOCUS
DEFINITION

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cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 CCTCATGC 1885
|||||
DB 8 CCTCGTGC 1

RESULT 125
CF323889
LOCUS
DEFINITION

HDN--05-A16_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 CCTCATGC 1885
|||||
DB 8 CCTCGTGC 1

RESULT 125
CF323889
LOCUS
DEFINITION

HDN--05-A16_g1 OshDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A16, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

cDNA library II (HDN) Oryza sativa cDNA clone HDN-06-H05, mRNA sequence.
 CF324406
 VERSION
 CF324406.1 GI:33797080
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 SOURCE
 ORGANISM
 Oryza sativa
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 1 (bases 1 to 8)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match 0.3%; Score 6.4; DB 1; Length 8;
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QY 1878 CCTCATGC 1885

Db 8 CCTCGTGC 1

RESULT 129
 CF325379
 LOCUS
 DEFINITION
 JMT1--03-B08-g1 AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-B08, mRNA sequence.

ACCESSION
 VERSION
 CF325379.1 GI:33799039
 EST.
 SOURCE
 ORGANISM
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 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 8)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

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Location/Qualifiers
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Query Match 0.3%; Score 6.4; DB 1; Length 8;
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QY 827 GCACGAGG 834

Db 1 GCACGAGG 8

RESULT 130
 CF325379/c
 LOCUS
 DEFINITION

CF325379
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 ACCESSION
 VERSION
 CF325379.1 GI:33799039
 EST.
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

1..8

Location/Qualifiers
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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 131
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DEFINITION JMT1--03-F06.g1 AtJMT-overexpressing transgenic rice lambda phage
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            sequence.
ACCESSION  CF325469.1 GI:33799223
VERSION     CF325469
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SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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                methyltransferase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 133
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DEFINITION JMT1--03-F22.g1 AtJMT-overexpressing transgenic rice lambda phage
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ACCESSION  CF325485.1 GI:33799255
VERSION     CF325485
KEYWORDS    EST.
SOURCE      Oryza sativa
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            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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                methyltransferase overexpression line."

Query Match      0.3%; Score 6.4; DB 1; Length 8;
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Qy 827 GCACGAGG 834
Db 1 GCACGAGG 8

RESULT 132
CF325469/c
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DEFINITION JMT1--03-F06.g1 AtJMT-overexpressing transgenic rice lambda phage
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ACCESSION  CF325469.1 GI:33799223
VERSION     CF325469
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SOURCE      Oryza sativa
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REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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TITLE       Large-scale Sequencing Analysis of Rice ESTs
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            Tel: 82 31 330 6193
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            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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                prepared from Arabidopsis Jasmonate Carboxyl
                methyltransferase overexpression line."

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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JOURNAL     Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1878 CCTCATGC 1885
Db 8 CCTCGTGC 1

RESULT 133
CF325485
LOCUS      CF325485      8 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT1--03-F22.g1 AtJMT-overexpressing transgenic rice lambda phage
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ACCESSION  CF325485.1 GI:33799255
VERSION     CF325485
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SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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REFERENCE   1 (bases 1 to 8)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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methyltransferase overexpression line."

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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 827 GCACGAG 834
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DB 1 GCACGAG 8

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RESULT 134
CF325485/c
LOCUS
DEFINITION
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sequence.
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CF325485
VERSION
CF325485.1 GI:33799255
KEYWORDS
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ORGANISM
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Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1878 CCTCATGC 1885
    |||||
DB 8 CCTCATGC 1

```

```

RESULT 135
CF338362/c
LOCUS
DEFINITION
Oryza sativa CDNA clone RCL1--01-H06, mRNA sequence.
ACCESSION
CF338362
VERSION
CF338362.1 GI:33825117
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8

```

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FEATURES
source
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="RCL1--01-H06"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli SOLR"
    /clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
    /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

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```

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1169 CCAACTTT 1176
    |||||
DB 8 CCAGCTTT 1

```

```

RESULT 136
CF339016/c
LOCUS
DEFINITION
Oryza sativa CDNA clone RCL1--03-111, mRNA sequence.
ACCESSION
CF339016
VERSION
CF339016.1 GI:33826415
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1169 CCAACTTT 1176
    |||||
DB 8 CCAGCTTT 1

```

```

RESULT 136
CF339016/c
LOCUS
DEFINITION
Oryza sativa CDNA clone RCL1--03-111, mRNA sequence.
ACCESSION
CF339016
VERSION
CF339016.1 GI:33826415
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza.
REFERENCE
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

Query Match      0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1878 CCTCATGC 1885
    |||||
DB 8 CCTCATGC 1

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-111"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1169 CCAACTTT 1176
||| ||||
Db 8 CCAGCTTT 1

RESULT 137

CF339699/c

LOCUS

DEFINITION RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--05-K22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--05-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

Query Match 0.3%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1169 CCAACTTT 1176
||| ||||
Db 8 CCAGCTTT 1

RESULT 138

CF340204/c

LOCUS

DEFINITION RCL1--07-E15.g1 Regenerated callus lambda phage cDNA library (RCL1)
Oryza sativa cDNA clone RCL1--07-E15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match

0.3%; Score 6.4; DB 1; Length 8;

Best Local Similarity 87.5%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1169 CCAACTTT 1176

||| ||||

Db 8 CCAGCTTT 1

RESULT 139

CF921494/c

LOCUS

DEFINITION GmRRwv3-10_B07_1_061 Soybean root hair subtracted cDNA library
GmRRwv3 Glycine max cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

CF921494 8 bp mRNA linear EST 05-NOV-2003
GmRRwv3 Glycine max cDNA, mRNA sequence.
CF921494
CF921494.1 GI:38192288
EST.
Glycine max (soybean)

ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 8)
 Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
 Expressed sequence tags from soybean root hair subtractive cDNA
 library
 Unpublished (2003)
 CONTACT: Gary Stacey
 University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752
 Fax: 573-882-0388
 Email: stacey@missouri.edu
 Single pass sequence
 Seq primer: T7

FEATURES
 source
 1..8
 Location/Qualifiers

/organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /issue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library
 gmrHw3"
 /note="Organ: root hairs; Vector: pCR2-1 Topo; cDNA clones
 generated from soybean root hair tissue treated with
 Bradyrhizobium japonicum for 3 hours."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 734 AGAACACAG 741
 Db 8 AAAACAG 1

RESULT 140
 CA794554
 LOCUS
 DEFINITION
 Cac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
 ACCESSION
 CA794554
 VERSION
 CA794554.1 GI:26051630
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 AUTHORS
 Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
 Retzel,E.R. and Jones,C.A.
 TITLE
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 1 (bases 1 to 8)
 Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
 Retzel,E.R. and Jones,C.A.
 JOURNAL
 Planta 216 (2), 255-264 (2002)
 MEDLINE
 22337596
 PUBMED
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: T3

FEATURES
 source
 1..8
 Location/Qualifiers

/organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"

/db_xref="taxon:3641"
 /clone="Cac_BL_1496"
 /tissue_type="Mature leaf and mature bean"
 /cell_type="Whole organ"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
 Cacao)"
 /note="Vector: pBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 222 CAAATGGG 229
 Db 1 CAAAAGGG 8

RESULT 141
 CA794554/c

LOCUS
 DEFINITION
 Cac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
 ACCESSION
 CA794554
 VERSION
 CA794554.1 GI:26051630
 EST.
 SOURCE
 Theobroma cacao (cacao)
 ORGANISM
 Theobroma cacao
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 AUTHORS
 Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
 Retzel,E.R. and Jones,C.A.
 TITLE
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 1 (bases 1 to 8)
 Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
 Retzel,E.R. and Jones,C.A.
 JOURNAL
 Planta 216 (2), 255-264 (2002)
 MEDLINE
 22337596
 PUBMED
 12447539
 COMMENT
 Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: T3

FEATURES
 source
 1..8
 Location/Qualifiers

/organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"
 /db_xref="taxon:3641"
 /clone="Cac_BL_1496"
 /tissue_type="Mature leaf and mature bean"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
 Cacao)"
 /note="Vector: pBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

Query Match 0.3%; Score 6.4; DB 1; Length 8;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1886 CCGTTTTC 1893
 Db 8 CCGTTTTC 1

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RESULT 142
CA850813/c
LOCUS
DEFINITION
D06G10_G10_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
cDNA clone D06G10 5', mRNA sequence.
ACCESSION
CA850813
VERSION
CA850813.1
KEYWORDS
GI:33387606
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 9)
REFERENCE
Alkharouf, N.W., Khan, R. and Matthews, B.P.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL
COMMENT
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="cDNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D06G10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1957 CATAAGCA 1964
|||||
9 CATAAACA 2
Db

RESULT 143
CF323490/c
LOCUS
DEFINITION
HDN--03-P21.g1 OshDACL-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--03-P21, mRNA
sequence.
ACCESSION
CF323490
VERSION
CF323490.1
KEYWORDS
GI:33795236
SOURCE
EST.
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 9)
REFERENCE
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--03-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 CCTCATGC 1885
|||||
8 CCTCGTGC 1
Db

RESULT 144
CA794225/c
LOCUS
DEFINITION
Cac BL 1208 Cac BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac BL 1208 5', mRNA sequence.
ACCESSION
CA794225
VERSION
CA794225.1
KEYWORDS
GI:26051301
SOURCE
EST.
ORGANISM
Theobroma cacao (cacao)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eucosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 9)
REFERENCE
Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retzel, E.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
JOURNAL
MEDLINE
22337596
PUBMED
12447539
COMMENT
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.
Location/Qualifiers
1..9
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac BL 1208"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac BL (Bean and Leaf from Amelonardo type
Cacao)"
/notes="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

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Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 961 TACCAACG 968
   |||||
Db 8 TATCAACG 1

RESULT 145
LOCUS      CA850899
DEFINITION D07H02.014.15.ab1 cDNA Peking library 2, 4 day SCN3 linear EST 01-AUG-2003
            cDNA clone D07H02 5', mRNA sequence.
ACCESSION  CA850899
VERSION    CA850899.1 GI:33387692
KEYWORDS   Glycine max (soybean)
SOURCE     Glycine max
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE     Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL   Unpublished (2002)
COMMENT   Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharouf@ars.usda.gov.

FEATURES             source
     source
     1..9
     /organism="Glycine max"
     /mol_type="mRNA"
     /cultivar="Peking"
     /db_xref="taxon:3847"
     /clone="D07H02"
     /tissue_type="Roots"
     /dev_stage="Seedlings"
     /note="Vector: pBluescript SK-; cDNA clones from mRNA
     extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1222 CCCATCCT 1229
   |||||
Db 9 CCCATCAT 2

RESULT 147
LOCUS      CF307008
DEFINITION HDAL-05-H11.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library 1 (HDAL) Oryza sativa cDNA clone HDAL-05-H11, mRNA
            sequence.
ACCESSION  CF307008
VERSION    CF307008.1 GI:33678769
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..9
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
     /clone="HDAL-05-H11"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli SOLR"
     /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
     phage cDNA library 1 (HDAL)"
     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

```

```

AUTHORS   Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE     Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL   Unpublished (2002)
COMMENT   Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharouf@ars.usda.gov.

FEATURES             source
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     1..9
     /organism="Glycine max"
     /mol_type="mRNA"
     /cultivar="Peking"
     /db_xref="taxon:3847"
     /clone="D07H02"
     /tissue_type="Roots"
     /dev_stage="Seedlings"
     /note="Vector: pBluescript SK-; cDNA clones from mRNA
     extracted from Peking roots 2 and 4 days past invasion."

Query Match      0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1222 CCCATCCT 1229
   |||||
Db 9 CCCATCAT 2

RESULT 147
LOCUS      CF307008
DEFINITION HDAL-05-H11.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library 1 (HDAL) Oryza sativa cDNA clone HDAL-05-H11, mRNA
            sequence.
ACCESSION  CF307008
VERSION    CF307008.1 GI:33678769
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 9)
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnahm@gbio.com, bnahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..9
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     /mol_type="mRNA"
     /cultivar="Nackdong"
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     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli SOLR"
     /clone_lib="OsHDAC1-overexpressing transgenic rice lambda
     phage cDNA library 1 (HDAL)"
     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

```

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 827 GCACGAG 834
|||||

Db 1 GCACGAG 8

RESULT 148
CF307008/c

LOCUS HDAL-05-H11.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL-05-H11, mRNA sequence.
DEFINITION

ACCESSION CF307008

VERSION CF307008.1 GI:33678769

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL-05-H11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 CCTCGTC 1885
|||||

Db 8 CCTCGTC 1

RESULT 149
CF307092/c

LOCUS HDAL-05-L14.g1 OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL) Oryza sativa cDNA clone HDAL-05-L14, mRNA sequence.

ACCESSION

VERSION CF307092.1 GI:33678853

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL-05-L14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda phage CDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 6.4; DB 1; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1026 GGAGCTTG 1033
|||||

Db 8 GGAGCTG 1

RESULT 150

CF309109

LOCUS

DEFINITION

ABF-03-C20.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF-03-C20, mRNA sequence.

ACCESSION CF309109

VERSION CF309109.1 GI:33680870

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 9)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

```

source
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF-03-C20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 769 TTCTTCT 776
Db 2 TTCTTCT 9

RESULT 151
CF323636
LOCUS
DEFINITION
HDN--04-F24.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--04-F24, mRNA
sequence.
ACCESSION
CF323636
VERSION
CF323636.1 GI:33795531
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 746 CCGTGTGC 753
Db 8 CCGTGTGC 1

RESULT 153
CF325619
LOCUS
DEFINITION
JMT1--03-L16.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
sequence.
ACCESSION
CF325619
VERSION
CF325619.1 GI:33799518
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

```

```

QY 442 CACAAGG 449
Db 2 CACAAGG 9

RESULT 152
CF323636/c
LOCUS
DEFINITION
HDN--04-F24.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa cDNA clone HDN--04-F24, mRNA
sequence.
ACCESSION
CF323636
VERSION
CF323636.1 GI:33795531
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .9
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--04-F24"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
Query Match
Best Local Similarity 0.3%; Score 6.4; DB 1; Length 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 746 CCGTGTGC 753
Db 8 CCGTGTGC 1

RESULT 153
CF325619
LOCUS
DEFINITION
JMT1--03-L16.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-L16, mRNA
sequence.
ACCESSION
CF325619
VERSION
CF325619.1 GI:33799518
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

```


end, mRNA sequence.
 CK298980
 VERSION CK298980.1 GI:39886896
 KEYWORDS EST.
 ORGANISM Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 10)
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
 Staskiewicz, B., Jil, H. and Baker, B.
 Generation of EST sequences from *Nicotiana benthamiana*
 Unpublished (2003)
 Other ESTs: EST761693
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
 Location/Qualifiers
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 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NBMDJ48"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from *Nicotiana benthamiana*
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (*Pseudomonas syringae* pv *tomato* 12 hr;
Xanthomonas campestris pv *campestris* 12 hr, 18hr;
Pseudomonas syringae pv *phaseolicola* 18hr, and *Xanthomonas*
campestris pv *vesicatoria* 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

FEATURES

source

Query Match 0.3%; Score 6.4; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 AAAATAAT 420
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 Db 8 AAAAAAAT 1

RESULT 157
 BU238234/c
 LOCUS
 DEFINITION Descurainia sophia 11 bp mRNA linear EST 06-SEP-2002
 Descurainia sophia cDNA clone Ds01_01e11, mRNA sequence.
 BU238234
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Descurainia sophia
 Descurainia sophia
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
 1 (bases 1 to 11)
 Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
 Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
 Expressed Sequence Tags from Cold-Stressed *Descurainia sophia*
 Seedlings
 Unpublished (2001)
 Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
 C66, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
 Location/Qualifiers
 1..11
 /organism="Descurainia sophia"
 /mol_type="mRNA"
 /db_xref="taxon:89411"
 /clone="Ds01_01e11"
 /tissue_type="leaf, stem"
 /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
 /clone_lib="Ds01_AAFRC_ECRC_cold_stressed_Flixweed_seedling
 gs"
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site 1: Eco RI;
 Site 2: Xho I; Plants were grown for 1 month at 200C/16
 hrs light/day (average 8 leaves, 1 cm tall, weight
 0.02g/plant). Then they were exposed to 20C, 12 hrs
 light/day, for 1 week. Library prepared by C. Piche using
 Stratagene kit."

Query Match 0.3%; Score 6.4; DB 1; Length 11;
 Best Local Similarity 87.5%; Pred. No. 87;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 593 AGATCTCT 600
 |||||
 Db 8 AGTCTCT 1

RESULT 158
 CF543031
 LOCUS
 DEFINITION S015532-024-030-P02-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 024-030-P02 5-PRIME, mRNA sequence.
 CF543031
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Beta vulgaris
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
 Plate: 30 row: P column: 02
 Seq primer: SP6.
 Location/Qualifiers
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 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiVar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:936732"
 /db_xref="taxon:161934"
 /clone="024-030-P02"

FEATURES
 source

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/tissue type="leaf"
/lab_host="EMDH10B"
/clone_lib="WP1Z-ADIS-024-leaf"
/note="Vector: PCWSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

```

```

Query Match      0.3%; Score 6.2; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 90;
Matches      8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 76 GAGGAGGGGAG 86
    |||||
Db 1 GGGGGGGGGGG 11

```

```

RESULT 159
CF338362
LOCUS
DEFINITION
RCL1--01-H06.g1 Regenerated callus lambda phage cDNA library (RCL1)
ACCESSION
CF338362
VERSION
CF338362.1 GI:33825117
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--01-H06"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

```

```

Query Match      0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2068 AAGCTG 2073
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Db 2 AAGCTG 7

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FEATURES
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1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--01-H06"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

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Query Match      0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2068 AAGCTG 2073
    |||||
Db 2 AAGCTG 7

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```

RESULT 160
CF339016
LOCUS
DEFINITION
RCL1--03-111.g1 Regenerated callus lambda phage cDNA library (RCL1)

```

```

ACCESSION
CF339016
VERSION
CF339016.1 GI:33826415
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--03-111"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library
(RCL1)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"

```

```

Query Match      0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2068 AAGCTG 2073
    |||||
Db 2 AAGCTG 7

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```

RESULT 161
CF339699
LOCUS
DEFINITION
RCL1--05-K22.g1 Regenerated callus lambda phage cDNA library (RCL1)
ACCESSION
CF339699
VERSION
CF339699.1 GI:33827769
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

```

Query Match      0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2068 AAGCTG 2073
    |||||
Db 2 AAGCTG 7

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--05-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2068 AAGCTG 2073

Db 2 AAGCTG 7

RESULT 162

CF340204
LOCUS
DEFINITION
Oryza sativa CDNA clone RC11--07-E15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
1 (bases 1 to 8)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..8
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--07-E15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2068 AAGCTG 2073

Db 2 AAGCTG 7

RESULT 163

CA850825
LOCUS
DEFINITION
Oryza sativa CDNA clone DO6H10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA850825.1 GI:33387618
EST.
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 8)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

USDA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

Location/Qualifiers
1..8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="DO6H10"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

FEATURES

source
1..8
/organism="Glycine max"
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/clone="DO6H10"
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/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1848 GGGTGG 1853

Db 1 GGGTGG 6

RESULT 164

CA850825/c
LOCUS
DEFINITION
Oryza sativa CDNA clone DO6H10 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA850825.1 GI:33387618
EST.
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 8)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

USDA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 8)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

FEATURES

source

Location/Qualifiers

1..8

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D06H10"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

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Best Local Similarity 0.3%; Score 6; DB 1; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 CCACC 410

Db 6 CCACC 1

RESULT 165

LOCUS

CA851350 D12G08 N20.14.abl cDNA Peking library 2, 4 day SCN3 Glycine max

EST. 01-AUG-2003

CA851350 cDNA clone D12G08 5', mRNA sequence.

ACCESSION CA851350.1 GI:33388143

VERSION EST.

KEYWORDS Glycine max (soybean)

SOURCE Glycine max

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 8)

Alkharouf, N.W., Khan, R. and Matthews, B.F.

Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode

Unpublished (2002)

Contact: Alkharouf, N.W.

Soybean Genomics and Improvement Laboratory (SGIL)

US Department of Agriculture (USDA), ARS, PSI

Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,

USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

FEATURES

source

Location/Qualifiers

1..8

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="D12G08"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 2, 4 day SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA

extracted from Peking roots 2 and 4 days past invasion."

Query Match

Best Local Similarity 0.3%; Score 6; DB 1; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1064 ACCCAA 1069

Db 1 ACCCAA 6

RESULT 166

LOCUS

CF297970 7LEAF--01-C16.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

EST. 15-AUG-2003

CF297970 sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297970.1 GI:33669731

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongui University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..8

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--01-C16"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1233 GACAGC 1238

Db 3 GACAGC 8

RESULT 167

LOCUS

CF297970/c 7LEAF--01-C16.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

EST. 15-AUG-2003

CF297970 sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION CF297970.1 GI:33669731

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCTGTC 251

DB 8 GCTGTC 3

RESULT 168

CF313731

LOCUS HD--01-P12.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-P12, mRNA sequence.
CF313731

ACCESSION CF313731.1 GI:33685492

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .8
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
/clone="HD--01-P12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"

/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 945 TGGTTT 950

DB 2 TGGTTT 7

RESULT 169

CF330558

LOCUS

DEFINITION

CF330558

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .8

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--06-F04"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

1. .8

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

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/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--01-P12"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

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/organism="Oryza sativa"

/mol_type="mRNA"

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/db_xref="taxon:4530"

/clone="HD--01-P12"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Cryzeae; Oryza.
 REFERENCE 1 (bases 1 to 8)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 FEATURES
 source
 1..8
 /organism="Oryza sativa"
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 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--06-F04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 6; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCTGTC 251
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 Db 8 GCTGTC 3

Search completed: March 1, 2004, 15:41:46
 Job time : 2 secs